

GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.	1.1	1529	56.2	529	20	AY40902
OM protein - protein search, using sw model	1.2	618	22.7	671	23	ABG61535
Run on: March 26, 2003, 18:41:34 : Search time 75 Seconds (without alignment) 950.521 Million cell updates/sec	1.3	600.5	21.9	608	21	AB29621
Title: US-09-888-035A-2	1.4	595.5	20.8	649	22	ABB5364
Perfect score: 2722	1.5	565.5	20.8	673	23	AAE16770
Sequence: 1 MGMEVAAARLGALTTSDYA.....GRGFVPPSPGSPTEQSHGGR 535	1.6	565	20.8	727	22	ABB63651
Scoring table: BL003662	1.7	552	20.3	569	20	AY44016
Gapop 10.0 , Gapext 0.5	1.8	541.5	19.9	509	23	ABG90555
Searched: 908470 seqs., 133250620 residues	1.9	541.5	19.9	509	23	ABG63438
Total number of hits satisfying chosen parameters: 908470	2.0	541.5	19.9	526	22	AB29637
Minimum DB seq length: 0	2.1	539	19.8	631	23	AAO14196
Maximum DB seq length: 2000000000	2.2	533	19.6	633	20	AY44017
Post-processing: Maximum Match 0%	2.3	481	17.7	816	14	AAU14143
Listing first 45 summaries	2.4	479.5	17.6	834	18	ABW1325
Database : A_Geneseq_101002:*	2.5	475.5	17.5	518	22	ABG5504
1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*	2.6	448	16.5	707	23	AAO14204
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*	2.7	448	16.5	717	23	AAU85408
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*	2.8	439	16.1	325	20	AY410906
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*	2.9	425.5	15.6	605	22	AUQ2884
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*	3.0	416.5	15.3	664	22	AUQ2883
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*	3.1	369.5	13.6	273	22	AAU01607
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*	3.2	362	13.3	275	22	AAU01608
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*	3.3	350	12.9	315	22	AAM24062
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*	3.4	312	11.5	531	23	ABG91666
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*	3.5	303.5	11.1	359	22	AAU01581
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*	3.6	292.5	10.7	339	22	AAU0590
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*	3.7	292.5	10.7	339	22	ABG90591
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*	3.8	292.5	10.7	339	23	ABG63436
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*	3.9	292.5	10.7	339	23	ABG65337
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*	4.0	288	10.6	990	22	ABG29884
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*	4.1	285.5	10.5	1146	23	AGT79102
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*	4.2	284	10.4	707	22	AAM23715
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*	4.3	284	10.4	707	22	AAM23744
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*	4.4	273	10.0	232	20	AY440907
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*	4.5	252.5	9.3	511	22	ABG10934

ALIGNMENTS

RESULT 1	AAB11832	standard; Protein: 535 AA.
ID	AAB11832	
XX		
AC	AAB11832;	
XX		07-NOV-2000 (first entry)
DT		
XX		
DE	Rice	Na+/H+ antiporter, OsNHX1.
XX		
KW	OsNHX1; Na+/H+ antiporter; sodium/proton antiporter; countertransporter; active transport; rice; transgenic plant; salt-tolerance.	
KW		
XX		Oryza sativa.
OS		
XX	PN	WO200037644-A1.
XX		
PD	29-JUN-2000.	
XX		
PF	07-NOV-2000	99WO-IP07224.
XX		
PR	22-DEC-1998;	98JP-0365604.
XX		
XX		(NORO) JAPAN MIN AGRIC FORESTRY & FISHERIES.
PA		
XX		Fukuda A, Tanaka Y;
PI		
XX		WPT: 2000-442672/38.
DR		N-PSDB; AAA61876.
DR		DNA encoding a sodium ion and proton counter-transporter protein of rice origin for production of salt tolerant rice transformants -
PT		rice
PT		Arabidopsis thalia
PT		Physcomtrella pat

Preq. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query ID	Match Length	DB ID	Description
1	2722	100.0	535	21 AAB11832	Rice Na+/H+ antiporter Attilplex_gmelini N
2	2105.5	77.4	555	21 AAB2786	Protein regulating protein regulating
3	2103.5	77.3	540	22 AAB3252	Protein regulating protein regulating
4	2095.5	77.0	553	22 AAB3253	Arabidopsis thalia
5	2055.5	75.5	542	22 AAB3251	Protein regulating
6	2023.5	74.3	538	20 AAY0901	Arabidopsis thalia
7	1966	72.2	555	22 AAB3254	Protein regulating
8	1852.5	68.1	547	20 AAY0905	Arabidopsis thalia
9	1799.5	66.1	571	22 AAU2882	Arabidopsis thalia
10	1550.5	57.0	556	23 AAU78424	Physcomtrella pat

PS Claim 1a; Fig 1; 43pp; Japanese.
 XX This sequence represents a novel rice Na⁺/H⁺ antiporter
 CC (countertransporter), OsNHX1. The invention relates to OsNHX1 and
 CC nucleic acids which encode it; vectors, host cells and transgenic plants
 CC containing OsNHX1 nucleic acids; recombinant expression of OsNHX1; and
 CC antibodies which recognise OsNHX1. OsNHX1 nucleic acids are useful in the
 XX production of salt tolerant transgenic plants.

Sequence 535 AA;

Query Match 100.0%; Score 2722; DB 21; Length 535;
 Best Local Similarity 100.0%; Pred. No. 8.4e-271;
 Matches 353; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 NGMEVAARLGALEYTSDYASVSVINLVALACTVLGHLEENWVNNEITALLIGLC 60
 Db 1 NGMEVAARLGALEYTSDYASVSVINLVALACTVLGHLEENWVNNEITALLIGLC 60
 Qy 61 TGVVILLMTKGSSHLFVFSPSDLFFYLPLPTTENAGFQKKOFFRNENTITLFGAVGT 120
 Db 61 TGVVILLMTKGSSHLFVFSPSDLFFYLPLPTTENAGFQKKOFFRNENTITLFGAVGT 120
 Qy 121 MISFFTISIAIAIAIFSRMNIGCTLDVGDFELAIGAISATDSVCTLQLNQDETPFLYSLVE 180
 Db 121 MISFFTISIAIAIAIFSRMNIGCTLDVGDFELAIGAISATDSVCTLQLNQDETPFLYSLVE 180
 Qy 181 GEGVNDATSVTLNQNEFLVHFLGNFIFYFLSSFLGIVAGLISAYIK 240
 Db 181 GEGVNDATSVTLNQNEFLVHFLGNFIFYFLSSFLGIVAGLISAYIK 240
 Qy 241 KLYIGHSTDREVALMLMAYLSMLAELLDLSGLITVPGCITYMSHTWHNTBESSRTV 300
 Db 241 KLYIGHSTDREVALMLMAYLSMLAELLDLSGLITVPGCITYMSHTWHNTBESSRTV 300
 Qy 301 TKHAPATLTSFAETPLFLYGMDALDIKEWFAASDRPGKSGTISISSLGLVIGRAAFYF 360
 Db 301 TKHAPATLTSFAETPLFLYGMDALDIKEWFAASDRPGKSGTISISSLGLVIGRAAFYF 360
 Qy 361 PLSFLSNLTKAPNKTITWQQVTVWAGLARGAVSIALAYNKTFTRSGHTQLHGNAMIT 420
 Db 361 PLSFLSNLTKAPNKTITWQQVTVWAGLARGAVSIALAYNKTFTRSGHTQLHGNAMIT 420
 Qy 421 STITVLFSTMVGFMATKPKLIRLLPASGHPTSEPPSSPKSLHSPLLTSMGSDLESTIN 480
 Db 421 STITVLFSTMVGFMATKPKLIRLLPASGHPTSEPPSSPKSLHSPLLTSMGSDLESTIN 480
 Qy 481 IVRPPSSLRMLLTKPTHTVHYYWRKEDDALMRPMFGRGFVFPSPGSPTEQSHGGR 535
 Db 481 IVRPPSSLRMLLTKPTHTVHYYWRKEDDALMRPMFGRGFVFPSPGSPTEQSHGGR 535
 RESULT 2
 AAB12786 DE Atiplex gmelini Na⁺ and H⁺ antiporter protein.
 XX ID AAB12786 standard; Protein; 555 AA.
 XX AC AAB12786;
 XX DT 23-NOV-2000 (first entry)
 XX DE Atiplex gmelini Na⁺ and H⁺ antiporter protein.
 XX KW Atiplex gmelini; Na plus and H plus antiporter protein;
 KW Na⁺ and H⁺ antiporter protein; transformed plant; high salt tolerance.
 OS Atiplex gmelini.
 XX PN JP2000157287-A.
 XX PD 13-JUN-2000.
 XX PF 16-SEP-1999; 99JP-0261606.
 XX

PR 24-SEP-1998; 98JP-0269504.
 XX
 PA (SHOK) SHOKUBUTSU KOGAKU KK.
 XX DR WPI: 2000-468209/41.
 DR N-PSDB; AAA2926.
 XX PT An Na⁺ and H⁺ plus antiporter protein and a gene encoding it -
 XX Disclosure; Page 10-12; 16pp; Japanese.
 PS
 XX
 CC The present sequence represents an Na⁺ and H⁺ antiporter protein
 CC isolated from Atiplex gmelini. The Na⁺ and H⁺ antiporter protein and
 CC gene encoding it are useful for the preparation of transformed plants
 CC with high salt tolerance, e.g. for growth in arid land.
 XX
 SQ Sequence 555 AA:
 Query Match 7.4%; Score 2105.5; DB 21; Length 555;
 Best Local Similarity 6.1%; Pred. No. 2.2e-207;
 Matches 410; Conservative 53; Mismatches 61; Indels 15; Gaps 4;
 Qy 7 AARLGAIYTTSDDASYSVSINLEVALLCATTYVNLQNEITLIGLCTGVIL 66
 Db 10 SGKMDAL-TISDHASVYSSMNLVALLGCVTIVGHLEENRMNESITALLIGL 68
 Qy 67 LMTKGKSHLFLVFSEDLFFTYLPLPLTENAGFQVKKKOFFRNEMTTLFGAVGTMSFFT 126
 Db 69 LISGGKSHLFLVFSEDLFFTYLPLPLTENAGFQVKKKOFFRNEMTTLFGAVGTMSFFT 128
 Qy 127 ISIAATAIFSRMNIGCTLDVGDFELAIGAISATDSVCTLQLNQDETPFLYSLVEGVVN 186
 Db 129 ISLGAISLKFQDGLTGLEADYLAIKAIFATDSVCTLQLNQDETPFLYSLVEGVVN 188
 Qy 187 DATSIVTENALQNEDLVHTDAVVLKFLGIVAGLISAYIKLYTIGR 246
 Db 189 DATSIVTENALQNEDLVHTDAVVLKFLGIVAGLISAYIKLYTIGR 248
 Qy 247 HSTDREVALMLMAYLSMLAELLDLSGLITVPGCITYMSHTWHNTBESSRTVTKHAF 306
 Db 249 HSTDREVALMLMAYLSMLAELDYLSMLAELDLSGLITVPGCITYMSHTWHNTBESSRTVTKHAF 308
 Qy 307 TLSFIAETEFLFYVMDALDIKEWFAASDRPGKSGTISISSLGLVIGRAAFYFPLSFLS 366
 Db 309 TLSFIAETEFLFYVMDALDIKEWFAASDRPGKSGTISISSLGLVIGRAAFYFPLSFLS 368
 Qy 367 NLTKKAPNEKITWQQVTVWAGLARGAVSIALAYNKTFTRSGHTQLHGNAMITSTTVY 426
 Db 369 NEAKKSQEKVTINQVITWAGLARGAVSIALAYNKTFTRSGHTQLHGNAMITSTVV 428
 Qy 427 LFSTMVFGMMTKPLIRLLPAASH -- -PVTESEPPSSPKSLHSPLLTSMQSDL--- 475
 Db 429 LFSTMVFGMMTKPLIRLLPAASH -- -PVTESEPPSSPKSLHSPLLTSMQSDL---
 QY 476 ESTT -- NIVRPPSSLRMLLTKPTHTVHYYWRKEDDALMRPMFGRGFVFPSPGSPTEQS 531
 DB 489 EDTTEPRTIVRPPSSLRMLLNAPHTVHYYWRKEDDALMRPMFGRGFVFPSPGSPTEQS 547
 RESULT 3
 AAB73252
 ID AAB73252 standard; Protein; 540 AA.
 XX AC AAB73252;
 XX DT 14-MAY-2001 (first entry)
 XX DE Protein regulating the pH of vacuoles.
 XX KW Vacuole pH regulation; flower colour.
 XX OS Petunia hybrida.

RESULT 4							
W0200114560-A1.	AAB73253	standard;	protein;	553	AA.		
XX	ID	AAB73253					
PD	XX						
01-MAR-2001.	XX						
XXX	AC	AAB73253;					
PPF	XX						
24-AUG-1999;	DT	14-MAY-2001	(first entry)				
PRR	XX						
24-AUG-2000;	DE	Protein regulating the pH of vacuoles.					
PA	XX						
(SUNR) SUNTORY LTD.	XX						
XXX	KW	Vacuole pH regulation; flower colour.					
PI	XX						
Iida S, Tanaka S, Inagaki Y;	OS	Nierembergia hybrida.					
XXX	OS						
DR	XX						
WPI; 2001-191648/19.	XX						
N-PSDB; AAF75764.	XX						
Morning glory-originated gene encoding a protein with pH regulation activity in vacuoles, useful in controlling flower color to give new breeds of colorful plants for cut flowers, particularly applicable in horticulture	PT						
XX	XX						
PS	XX						
Example 7; Page 42-45; 68pp; Japanese.	XX						
CC	XX						
The present sequence is a protein, which has vacuolar pH regulatory activities. The protein enables flower colour to be controlled via regulation of the vacuolar pH, colours can range from blue to red in colour spectrum. The protein is useful in controlling flower colour to give new breeds of colourful plants for cut flowers, particularly applicable in horticulture.	CC						
XX	CC						
SO	XX						
Sequence 540 AA;	SO						
Query Match 77.3%; Score 2103.5; DB 22; Length 540;	SO						
Best Local Similarity 77.4%; Pred. No. 3.4e-207;	SO						
Matches 404; Conservative 53; Mismatches 62; Indels 3; Gaps 1;	SO						
Qy 15 TTSYASVSVINLEVALICAVIGHLEENRNNESTALIGLCTGVVILMKGSS 74	Qy						
Db 16 STSDHQSVSVINLEVALICAVIGHLEENRNNESTALIGVSCGIVILLISGGNS 75	Db						
Qy 75 HLFVFSEDLFIFYLPLPPIIFAGQVKKKOFFNEMTITLGAVGTMSIFTSTIAATAI 134	Qy						
Db 76 HLFVFSEDLFIFYLPLPPIIFAGQVKKKOFFNEMTITLGAVGTMSIFTSTIAIGT 135	Db						
Qy 135 FSRMNIGTLDVGDFELAIGAIFASATDSVCTLQLVNQDETFLPFLYSLVFGEVNDATSTIVLF 194	Qy						
Db 136 FKKNMIGSLIEDGYLAIGAIFASATDSVCTLQLVNQDETFLPFLYSLVFGEVNDATSVVLF 195	Db						
Qy 195 NALONFDLVHDAAVLKFQGNFYLFLSSTFLGVAGLSSAYIKKLYGRHSTDREVA 254	Qy						
Db 196 NALONFDLSHDTGKAMELVNFYLFLASSTALGAAGLSSAYIKKLYGRHSTDREVA 255	Db						
Qy 255 LMMMAUAYSLMLAELLDLSGLITYTFFCGITMSHTWHNTYESSRVTTKAFAFLSFIATP 314	Qy						
Db 256 IMIMAYLSSMLAELFYSLAAYNTRSGHTQLQIGNAIMTSTIVLLESTMVFG 315	Db						
Qy 315 FFLYVGMDAALDIEKWEFASDRPGKSIGTISIISLLGLVLIGRAAEVFLPSLNSLUTKKAPN 374	Qy						
Db 316 AKISFNQVQTWWAGLMRGAVSAMALAYNQTRGGHTQLRANAIMTSTIVLLESTVVFG 375	Db						
Qy 375 EK1TWROQVTTWWAGLMRGAVSAMALAYNQTRGGHTQLRANAIMTSTIVLLESTMVFG 434	Qy						
Db 376 AKISFNQVQTWWAGLMRGAVSAMALAYNQTRGGHTQLRANAIMTSTIVLLESTVVFG 435	Db						
Qy 435 MMTPKLIRULLPASGH-- PVTSESPSSPKSLHSPLSLTSMQGSDLESTNNVRPSSLRMLL 491	Qy						
Db 436 LMTRPLIRULLPSSRHLRMSSEPTTPRSFIVPLUDSTDSEADLERHVRPHSLRMLL 495	Db						
Qy 492 TKPHTHYYWRKFEADDALMRPMEEGRGEVFPSPGSPTEQSHG 533	Qy						
Db 496 STPSHTVHYWRKFDNAFRPVFGGRGEVFPAGSPTDPVFG 537	Db						
Qy 315 FFLYGMDDALDIEKWEFASDRPGKSIGTISIISLLGLVLIGRAAEVFLPSLNSLUTKKAPN 374	Qy						
Db 316 FFLYGMDDALDIEKWEFASDRPGKSIGTISIISLLGLVLIGRAAEVFLPSLNSLUTKKAPNPE 375	Db						
Qy 375 EK1TWROQVTTWWAGLMRGAVSAMALAYNQTRGGHTQLRANAIMTSTIVLLESTMVFG 434	Qy						
Db 376 AKISFNQVQTWWAGLMRGAVSAMALAYNQTRGGHTQLRANAIMTSTIVLLESTVVFG 435	Db						
Qy 435 MMTPKLIRULLPASGH-- PVTSESPSSPKSLHSPLSLTSMQGSDLESTNNVRPSSLRMLL 491	Qy						
Db 436 LMTRPLIRULLPSSRHLRMSSEPTTPRSFIVPLUDSTDSEADLERHVRPHSLRMLL 495	Db						
Qy 492 TKPHTHYYWRKFEADDALMRPMEEGRGEVFPSPGSPTEQSHG 533	Qy						
Db 496 STPSHTVHYWRKFDNAFRPVFGGRGEVFPAGSPTDPVFG 537	Db						

This would be useful in farming land in areas that are generally considered unproductive through salt accumulation and poor irrigation, e.g. in India, Australia, and prairies in USA or Canada. Commercial crops, such as potatoes, tomatoes, brassica, cotton, sunflower, strawberries, spinach, lettuce, rice, soybean, corn, wheat, rye, barley, amaranth, sorghum, alliaria, saicornia and others would benefit from increased salt tolerance.

PA (SUNR) SUNTORY LTD.
 XX
 PI Iida S, Tanaka S,
 XX
 DR WPL: 2001-191648/19.
 N-PSDB; AAF75766.
 XX

XX	DT	18-JAN-2000	(first entry)	QY	243	YIGRHSTDREVALMMAYLSYMELLDLSGLTIVFFCGTIVMSHYWHNVTESRSRVTK	302
XX	DE	Arabidopsis thaliana Na/H transporter.		Db	241	YFGRHSTUREVALMMAYLSYMELLDLSGLTIVFFCGTIVMSHYWHNVTESRSRVTK	300
XX	KW	Sodium; proton; antiport; transporter; salt tolerance; salt management; transgenic plant; survival; soil; farming; accumulation; irrigation; crop.		QY	303	HATATLSFAETEFLYYGMDALDIKEWEEASDRPGKSIGISSLGLVIGRAAFVFPL	362
XX	KW			Db	301	HTATLSFAETEFLYYGMDALDIKEWEEASDRPGKSIGISSLGLVIGRAAFVFPL	360
XX	OS	Arabidopsis thaliana.		QY	363	SFLSNLTKKAPNEKTIWROQVVIWAGLMRGAVSIALAYNKFRSGTOLGNAIMTST	422
XX	PN	W09947679-A2.		Db	361	SFLSNLAKKNQSKRINFNMQVVIWAGLMRGAVSIALAYNKFRSGTOLGNAIMTST	420
XX	PD	23-SEP-1999.		QY	423	ITVVLFSTMVEGMMTKPLIRLLPASHPVT - SEPPSSPKSLHSPLTSMQSDLESTTN	480
XX	PF	18-MAR-1999;	99WO-CA000219.	QY	481	IVRPSSLLEMILJTKPT	495
XX	PR	18-MAR-1998;	98US-0078474.	Db	421	ITVCLFLSTVFGMLTKPLISYLUPLQHNAATTSMISDDNNPKSHIPLDQSDTEPSENHN	490
XX	PR	15-JAN-1999;	99US-0116111.	Db	481	VPRPDSTRGELTRPT	495
PA	(BLUM/)	BLUMWALD E.		RESULT 9			
PA	(APSE/)	APSE M.		AAU02882			
PA	(SNED/)	SNEDDEN W.		ID	AAU02882 standard	protein:	571 AA.
PA	(AHAR/)	AHARON G.		XX			
PI	XX	Blumwald E., Apse M., Snedden W., Aharon G;		AC	AAU02882;		
DR	XX			XX	12-SEP-2001 (first entry)		
N-PSDB;	XX			DE			
AA22595.	XX			XX	Arabidopsis thaliana AtNHX1 polypeptide.		
PT	XX			KW	AtNHX1; tonoplast pyrophosphatase hydrogen ion translocating pump; Avp1; vacuolar pyrophosphatase; salt tolerance; sodium; calcium; manganese; lead; saline soil; thale-cress.		
PT	XX			KW	freeze tolerance; 35S promoter; sodium; calcium; manganese; lead; saline soil; thale-cress.		
PS	XX			OS	Arabidopsis thaliana.		
PS	XX			XX	PN	W200133945-Al.	
DR	XX			PD	17-MAY-2001		
WPI: 1999-571840/48.	XX			XX	10-NOV-2000;	2000WO-US30955.	
N-PSDB;	XX			PF	10-NOV-1999;	99US-0164808.	
AA22595.	XX			PR	10-AUG-2000;	2000US-026223.	
XX	PT			PR	22-AUG-2000;	2000US-0644039.	
PT	XX			XX	(UYCO) UNIV CONNECTICUT.		
PS	XX			PA	(WHED) WHITEHEAD INST.		
CC	XX	The invention relates to an isolated nucleic acid molecule encoding a plant Na/H antiport (PNX) transporter polypeptide, or a fragment and capable of increasing salt tolerance in a cell. This sequence corresponds to a transporter from Arabidopsis thaliana.		XX	Gaiola RA;		
CC	CC	The Na/H transporter polypeptides provide means of intracellular salt management, particularly in plants. The sequences are useful for producing transgenic plants that are capable of surviving in soil with high salt levels that would normally inhibit growth of the crop species. This would be useful in farming land in areas that are generally considered unproductive through salt accumulation and poor irrigation, e.g. in India, Australia, and prairies in USA or Canada. Commercial crops, such as potatoes, tomatoes, brassica, cotton, sunflower, strawberries, spinach, lettuce, rice, soybean, corn, wheat, rye, barley, atriplex, sorghum, alfalfa, salicornia and others would benefit from increased salt tolerance.		PD	PI		
CC	CC	Sequence 547 AA;		XX	XX		
CC	CC	Query Match 68.1%; Score 1852.5; DB 20; Length 547;		DR	WPI: 2001-328862/34.		
Best Local Similarity 72.3%; Pred. No. 2.2e-181;	Matches 361; Conservative 55; Mismatches 76; Indels 3; Gaps 2;			XX			
QY	3	MEVAARLGAATTSYDAYSVSINLVALICACIVLGHILENRWNENSTALLIGCNG	62	PT	Transgenic plants with salt tolerance, drought and freeze resistance		
Db	2	LDSLVSKLGSLS-STS DHASV ALNLVALICACIVLGHILENRWNENSTALLIGCNG	60	PT	and increased yield and flower size comprise exogenous H ⁺ genes or increased vacuolar pyrophosphatase expression -		
QY	63	VVILLMTKGSKSHFVSEDFFLYLPPPTENAGFOVKKKOFFRNEMITLFGAVGTM	122	XX	Example 1; Fig 6: 68pp; English.		
Db	61	VILLISKGSKSHLVLFSDFLFLYLPPPTENAGFOVKKKOFFRNEMITLFGAVGTM	120	CC	The sequence represents an Arabidopsis thaliana AtNHX1 polypeptide which is a tonoplast pyrophosphatase hydrogen ion (H ⁺) translocating pump.		
QY	123	SFFTTISIAIAIFSRMIGLTDVCFDLAIGAIFSATDSVCTLYQLNQDETFLYSLVGE	182	CC	Transgenic plants can be made by transforming plant cells with exogenous CC tonoplast pyrophosphate driven H ⁺ pump genes and an exogenous nucleic CC acid encoding a protein, such as Avp1, which alters expression of CC vacuolar pyrophosphatase. Salt tolerance may be introduced into a plant CC via transformation of the cells to induce upregulation of vacuolar CC pyrophosphatase expression. Drought and/or freeze tolerance may also be CC introduced through transformation with DNA encoding a vacuolar H ⁺ CC translocating pump linked to a promoter such as the 35S promoter. These CC processes are useful for bioremediating soil and removing cations such as CC sodium, calcium, manganese and lead from soil or water which can		
Db	121	SCTTISLGTVQQFKKLDCIGFLDGDYLAIGAIFAATDSVCTLYQLNQDETFLYSLVGE	180	CC			
QY	183	GVNDATSLVFLNALQNFDLVHIDAAVVLKFLGNFNFYLFLSSTFLGVAGLSSAYIKKL	242	CC			
Db	181	GYVNDATSVVFNQFNLQAFHLGNFLYFLFLLGAAATGLISAYVIKKL	240	CC			

CC support plant growth. Plants which grow in saline soil can be produced
CC and yield and flower size of plants can be increased.

PA (BADI) BASF PLANT SCI GMBH.
XX PI Da Costa Silva EO, Ishitani M;

SQ Sequence 571 AA;
Score 66.18; Score 1799.5; DB 22; Length 571;
Best Local Similarity 68.3%; Pred. No. 6.6e-176; Matches 364; Conservative 62; Mismatches 100; Indels 7; Gaps 4;

Qy : 3 MEVAARLGLAATTSYASVVSINLFLVALICACTIVLGHILEENRWNVESITALLIGLCTG 62
Db 2 LDSLVSKPLSL-STSDHASYVALNLPVALICACTIVLGHILEENRWNMKSSITALLIGLCTG 60

Qy 63 VVILLMTKGKSHLVEFSEDFIIFTYLPLPTIFNAGFQVKKKQFRNFMITLFGAVGTM 122
Db 61 VTLILISKGKSHLVEFSEDFIIFTYLPLPTIPNAFQVKKKQFRNFMITLFGAVGTM 120

Qy 123 SFTTISTATAIFSRMNTIGLTDGFELAIAFSAATSVCTLQLVNQDTEPFLYSLYFC 182
Db 121 SCTTISUCVTQFPKKLDIGTDFDCYLACIAFAATDSYCTLQLVNQDTEPFLYSLYFC 180

Qy 183 GVNDATSIVFLNALQNFIDLVHDAAVVFLGLNFYFLFUSLSTFLGVFLGAGLLSAYTIKRL 242
Db 181 CVDNDATSVVFNATQSDFLTHNRAAFHILCNFLYFLSTLGAACLISAYVIKRL 240

Qy 243 YIGRHSTDREVALMMALYSYMIAELDLISGLITVFFCGIVMSHYTWINVTESSRTIK 302
Db 241 YFCRHSDTRVYALMMALYSYMIALRFDLSCILTVPCFGVMSHYTWINVTESSRTIK 300

Qy 303 HAFATLSFIAETFLFLYVGMDALDIEKWEFASDRDGKSIGISSITLGLIGRAFAFVFPPL 362
Db 301 HTFATLSFLARPFLFLYVCMDALDIDKWRVSDDTPTSIASVSLMLGVNGRAFAFVFPPL 360

Qy 363 SPLSNLTKAPNEKITWRRQQVIVIWAQLMRCAVSTALAKKFTRAGHTQHLGNAIMITST 422
Db 361 SPLSNLAKNQNSRKTNEMQVIVIWSGLMRCAVSMALAKKFTRAGHTQHVGNALIMITST 420

Qy 423 ITVVLFSTMVFGMMTKPLIRLILPASHPVTT--SEPPSPKSLSHSPLTSMQSDLEST- 479

Db 421 ITVCLFSTVVFCMLTKPLISVILPHONATISMLSDDNTTPSIIHFLD--QDSFTEPSCN 478

Qy 480 -NTVRPSSLRMUMLTKPTHTVHYYWRFKDALMRPMFGRGFVFPFSGPSPBEQS 531
Db 479 HNPVRPDSSRGFLTRPTRVHYYWRFQDFDSMPVFCCRGFVFPFGSPTERN 531

RESULT 10
AAU78424 standard; Protein: 556 AA.
ID AAU78424
XX AC AAU78424;
XX DT 18-JUN-2002 (first entry)
XX DE Physcomtrella patens Na+/H+ antiporter PPNHX1.
KW Plant; Na+/H+ antiporter; PPNHX1; expressed sequence tag; EST;
KW plant protectant; cytosatic; stress tolerance; plant defence activity;
KW cancer; gall; tumour; suppressor; pathogenic stress; herbicide;
KW insecticide; acid rain; drought tolerance; plant hormone synthesis;
KW ultraviolet tolerance; flower development; terpene synthesis;
KW plant organoleptic.
XX OS Physcomtrella patens.
XX PN WO200216423-A2.
XX PD 28-FEB-2002.
XX PR 24-AUG-2001; 2001WO-US56550.
XX PR 25-AUG-2000; 2000US-227974P.

PA (BADI) BASF PLANT SCI GMBH.
XX PI Da Costa Silva EO, Ishitani M;
XX DR WPI: 2002-292058/33.
PT New Na+/H+ antiporter nucleic acids and proteins, useful e.g. for modulating stress tolerance in plants, or for detecting, preventing, conferring resistance to or treating hyperproliferative diseases, e.g. cankers, galls or tumours -
PS Claim 1; Fig 3; 204pp; English.
XX The invention relates to novel isolated Na+/H+ antiporter coding nucleic acid (I) and polypeptides (II). (I) and (II) are useful in modulating the stress tolerance in a plant, preferably modulating a plant's tolerance to limited or inadequate water availability, excess salt or osmotic conditions, excess temperature conditions, excess metal concentration in soil or water, chemical stress and oxidative stress. These may also be used as carbon, nitrogen or carbohydrate source, in modulating plant defence activity, signal transduction, or metabolite transport; or as probes for the identification and isolation of full length cDNAs or genomic DNA. The polynucleotides or polypeptides are further used to detect, prevent, confer resistance to and/or treat hyperproliferative diseases such as cancers, galls, tumours, and appressorium, increase plant defence mechanisms against environmental or pathogenic stresses (e.g. viral, fungal, mycoplasma, bacterial, nemate, herbicidal, insecticidal, acid rain, drought, or chemical), and hormone synthesis. The Na+/H+ antiporter coding nucleic acids can be used in creating transgenic plants with desirable traits, including enhanced plant defence, drought tolerance, ultraviolet tolerance, salt tolerance, enhanced flower development and terpene synthesis, in expressing recombinant proteins to raise antibodies against polypeptides, as markers for tissues in which the corresponding protein is expressed, as chromosome markers or tags for chromosome mapping, and for genetic fingerprinting. The polypeptides are useful in the identification, prevention, and/or confirmation of resistance to plant diseases, particularly those associated with modulating environmental stress responses, such as drought, freezing and salt tolerance. The polypeptides are further useful in modulating plant yield, development, differentiation, root growth, root morphology, plant colour, plant aroma, plant flavour, palatability or plant tissue, plant organoleptic properties, ability to serve as plant nutraceutical, pharmaceutical or phytochemical, ability to produce nutraceutical, pharmaceutical or phytochemicals of either endogenous or exogenous origin. Antibodies may be used in diagnostic assays to detect the presence or quantity of the polypeptides in affinity purification of the polypeptides from recombinant cell culture or natural sources, and for inhibiting allergic reactions in animals. The present sequence represents Physcomtrella patens Na+/H+ antiporter PPNHX1.
SQ Sequence 556 AA;
Query Match 57.0%; Score 1550.5; DB 23; Length 556;
Best Local Similarity 60.9%; Pred. No. 2.6e-150;
Matches 316; Conservative 66; Mismatches 116; Indels 21; Gaps 7;
Db 18 MNIGHTDVGDFLAIGAIISATDSVCTLQLVNQDETPFLYSLVFGVWVNDATSVLFNL 197
Db 23 DRDVISICLFEVFLCACIVLGHILEENRMNESITALLGLFIGSTVLISSKGQGSHL 82
Qy 78 VFSEDLIFFTYLPLPPTIFNAGFQVKKKQFFRNEMTITLFGAVGTMSEFTTISIAATIFSR 137
Db 83 EFDEELIFFTYLPLPPTIFNAGFQVKKEFFRNITIMFFGVTGFGTISTGQWYFISK 142
Qy 138 MNIGHTDVGDFLAIGAIISATDSVCTLQLVNQDETPFLYSLVFGVWVNDATSVLFNL 197
Db 143 FGLKNLPIRDILAIQVTSATDSVCTLQLVNQDETPFLYSLVFGVWVNDATSVLRSR 202
Qy 198 QNFDLVHDAAVFLGFLPFLSSTGUVFAGLSSATIKKLYIGRHSTDREVALM 257
Db 203 QTYNFDNFTSLEGQIIGGSFLYLFSSCILGIASGLISAYIKTMYFGRHSTDREIAIMT 262

strawberries, spinach, lettuce, rice, soybean, corn, wheat, rye, barley, attriplex, sorghum, alfalfa, salicornia and others would benefit from increased salt tolerance.	XX	Sequence	529 AA;
Query Match	56.2%	Score 1529;	DB 20; Length 529;
Best Local Similarity	58.2%	Pred. No. 3.9e-148;	
Matches	297;	Conservative	83; Mismatches 116; Indels 14; Gaps 5;
QY	17 SDYASVVSINLFWALLCACIVLGHLLEENFWVNESTALIGLCGVVILLMTGRSSH1 76		
Ddb	15 AEHPQVITSSVFAILCLCVLGHLEENFWVNESTALIGLCGVVILLMTGRSSH1 74		
Qy	77 FVESEDLIFYLPLIIPNAGFQVKKKPFRNEMTITLFGAVGMISFFFTSIAATAIFS 136		
Ddb	75 LVEDEEFLFYIPLIIPNAGFQVKKKPFHNLTTMSFEGIVGFLSTVLSFGTWMLFP 134		
Qy	137 RMNIGLTLDVGDFLAIGAFLSATSDSVCTLQVLYNQDETPEFLYSVLFEGVWVNDATSVLFLNA 196		
Ddb	135 KLGFKGSLARDYLAIGTIFSTSDVCTLQLHQDETPEFLYSVLFEGVWVNDATSVLFLNA 194		
Qy	197 LQNFDLVHDAAVVLLKELGNFFYFLFSSTFLGVFAGLSSYIIKKLYIGHSTDREVALM 256		
Ddb	195 VOKIQFESLVTGNTALQVFLNQFLYFLSTISLIGVGLTISFLVLTGFGRHSTRELAIM 254		
Qy	257 MMLAYSLYMLAELLDLSGLTIVFCGIYSHYTNVTESRVTKHAFATLSFLAETFI 316		
Ddb	255 VLMAYSLYMLAELFSLSGLTIVFCGVLMHSHASYNTVSSRSRTRSHFAMLSFLAETFI 314		
Qy	317 FLYVGMDALDIKEWFAFSDRPGKSIGISSLIGLVGRAFVFPLSFLSNTLKK--APN 374		
Ddb	315 FLYVGTDALDTWKWTKTSSLFSGGTLGVSFITALVLLGRAFAFPBLSVTFNMNRHTERN 374		
Qy	375 EKTWTROQQVVIWAGLMBGAVSTALAYNKPTRSGHTQHLGNAIMITSTITVVLFSTMVFG 434		
Ddb	375 ESTTEKIQVVIWAGLMBGAVSTALAKFOFTYSCVTLDPVNAAMVNTPTIVVLEFTLVFG 434		
Qy	435 MNTKPLFLRLPLDASGHPYT-----SEPSPK_SLSPLUTSMGDSLISSTNTIVRPS-SS 486		
Ddb	435 FLTKPLVNVLPQDASHNTGNGRKTEGSPKEDATLPLS---FDESASTNENRARDS 490		
Qy	487 LRMMLTKPTHTVHYWWRKFDDALMRPMFEG 516		
Ddb	491 ISLLMEQPVITYHYWWRKFDDTYMPPIFG 520		
	RESULT 12		
BGB6155	ABG6155 standard; Protein: 671 AA.		
X	ABG6135;		
X	ABG6135;		
X	27-AUG-2002 (first entry)		
X	Human transporter and ion channel, TRICH5, Incyte ID 7476938CD1.		
X	Human transporter and ion channel; TRICH5; transport disorder; cancer;		
X	neurological disorder; muscle disorder; immunological disorder; cell		
X	sclerodema; systemic lupus erythematosus; allergy; leukaemia; cell		
X	proliferative disorder; cervical cancer; breast cancer; neurodegenerative disorder; Parkinson's disease; Alzheimer's disease; myotonic dystrophy; catatonica; endocrine disorder; diabetes; Graves' disease; gastrointestinal disorder; Crohn's disease; renal disorder; Good pasture's syndrome; viral infection; cirrhosis; bacterial infection; fungal infection; parasitic infection; protozoal infection; helminthic infection; cardiovascular disorder; atherosclerosis; hepatic disease.		
X	Homo sapiens.		
X	WO200240541-A2.		

encoded proteins. The invention additionally encompasses expression constructs, recombinant viruses and recombinant cells comprising the nucleic acids of the invention, recombinant production of the proteins, antibodies against the proteins, a method of identifying inhibitors of the proteins, and compositions comprising the inhibitors for administration to an animal. The nucleic acids, and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with flea infestations. For example, the nucleic acids may be used to produce an HMT or HNC protein according to standard recombinant DNA methodology by inserting the nucleic acids into a host cell and culturing the cell to express the protein. The HMT and HNC nucleic acids may also be used as DNA probes in diagnostic assays (e.g., PCR) to detect and quantitate the presence of cat flea or other homologous nucleic acid sequences in samples. They may also be used to study the expression and function of the proteins and their role in metabolism. The HMT and HNC proteins may be used as antigens in the production of specific antibodies, and in assays to identify modulators (agonists and antagonists) of HMT and/or HNC protein expression and activity. The anti-HMT/HNC protein antibodies and antagonists may also be used to downregulate protein expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of flea polypeptides in samples (e.g., by enzyme linked immunosorbent assay (ELISA)). The present sequence represents a cat flea HMT protein of the invention.

Query Match	Score	DB	Length	Start
Best Local Similarity	600.5	DB 21;	608;	
Matches 153; Conservative 95; Mismatches 153;	Pred. No. 1.4e-52;			13;
	Gaps			
21 SVSINLEVALICACIVLGHILEEN - RWNVNSITALLIGLCTGVILLMTKGKSSHLL - 76				
81 SSMSIFFVLCVLAQGLLIPHMLQTGQFVKKQQFFNFMITLGAVGTMSIATIAAFLNNMSKNNVNKN 140				
77 -FVFSEDLFLFVLLPPLIFNAGFQVKKQQFFNFMITLGAVGTMSIATIAAFLNNMSKNNVNKN 140				
141 EEAESPTAFLVLLPPLIFEGSYNLHKGNFQNIGSILVFAFGTAISAFVVG AGVYL 199				
136 SRMNG-TLDVGDFELAIGAIFSATSVDSTQTLQVNLQ-DTFPIFLYSLVFGEGVVNDATSVIYL 193				
200 GMADVAYNLSFVEFSAGFSGLSIISAVDPEVATVAFHALDDPVNLMLVGEISILDAISTVIL 259				
194 FNA-LQNFDLVHIDAAVVLKFLGNFPFLSSTFLGYFAGLRLSAYLIKKLYIGRHSTDRE 252				
260 TTAVLESNNLMTTAAVSSGLNRFCLMFPSAGIGVFLVPSALLKHVDLKRYPS-E 318				
253 VALMMILMAYLSYMLAELLDDLSGILTVEFCGIVMSHYTHWNYTESSRVYTTHAFATLSEFA 312				
319 LGMMIVFTYAPVLAEGIHLGSMIAILFCGIVMSHYTHENLSTVTOITMQQTMRMLTAAFA 378				
313 ETFLFLYVGNDALDEKWEASDRPKSIGISSILGLVIGRAAFVFLPSLNULNTRKA 372				
379 ETCVAYFLGAIFSFRR----HRVEPAFLVWSIV -LCLIGRAANIFPLSWLVNOFRE- 429				
373 PNEKTTWROQSVIWWAGLGMGVASTALA --- YNKFTRSQHTQLHGNAIMITSTTIVYL 428				
430 -HKTTKKAPAFIMWESGL -RGAISYIALSLLFSDETRH ----- VITITLIIIVLC 477				
429 STMVFGMMTKPLIRLL 444				
478 TTLFGGATMPLKFL 493				
SULT 14				
ABBS59364 standard; Protein; 649 AA.				
ABBS59364;				

Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

Drosophila melanogaster.

WO2001171042-A2.

27-SEP-2001.

23-MAR-2001; 2001WO-US09231.

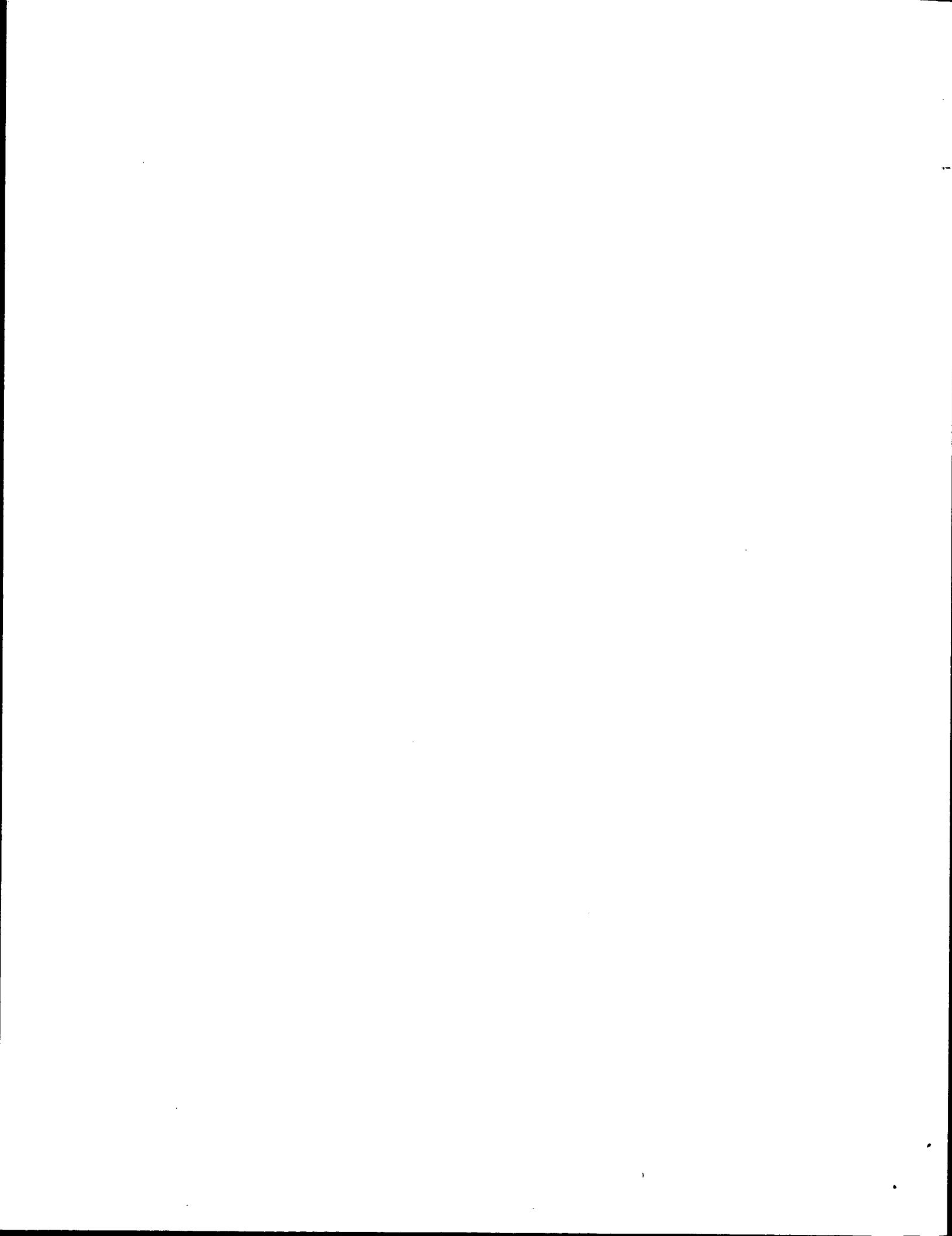
23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.

(PEKE) PE CORP NY.

Venter JC, Adams M, Li PWD, Myers EW;

WPI; 2001-656860/75.
N-PSDB; ABL03467.

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions.



GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 26, 2003, 18:51:14 : Search time 28 Seconds
(without alignments)
562.188 Million cell updates/sec

Title: US-09-888-035A-2

Perfect score: 2722

Sequence: 1 MGMEVAAAARGALYTTSDYA.....GRGFVPPGSPTEQSHGGR 535

Scoring table: Blosum62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : Issued_Patents_AA:
 1: /cgn2_6/pktodata/1/iaa/5A_COMBO.pep:
 2: /cgn2_6/pktodata/1/iaa/5B_COMBO.pep:
 3: /cgn2_6/pktodata/1/iaa/6A_COMBO.pep:
 4: /cgn2_6/pktodata/1/iaa/6B_COMBO.pep:
 5: /cgn2_6/pktodata/1/iaa/PCTUS_COMBO.pep:
 6: /cgn2_6/pktodata/1/iaa/backfile1.pep:
 Pred. No. is the number of results predicted to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	491	18.0	832	2	US-09-677-734A-12	Sequence 12, Appl
2	491	18.0	832	4	US-09-097-053-12	Sequence 12, Appl
3	482.5	17.7	834	2	US-08-677-734A-9	Sequence 9, Appl
4	482.5	17.7	834	2	US-08-677-734A-10	Sequence 9, Appl
5	482.5	17.7	834	4	US-09-097-053-9	Sequence 10, Appl
6	482.5	17.7	834	4	US-09-097-053-10	Sequence 11, Appl
7	480.5	17.7	831	4	US-09-097-053-11	Sequence 11, Appl
8	480.5	17.7	831	4	US-09-134-001C-5576	Sequence 5576, Appl
9	200.5	7.4	683	4	US-09-134-001C-5576	Sequence 11, Appl
10	130.5	4.8	635	2	US-09-014-969-11	Sequence 4125, Appl
11	124.5	4.6	605	4	US-09-134-001C-4425	Sequence 4125, Appl
12	118.5	4.4	800	4	US-09-134-001C-5655	Sequence 5655, Appl
13	114	4.2	477	4	US-09-134-001C-3487	Sequence 3487, Appl
14	113	4.2	1394	4	US-09-213-053-2	Sequence 2, Appl
15	111	4.1	650	4	US-08-800-291B-4	Sequence 4, Appl
16	110	4.0	400	4	US-09-134-001C-2912	Sequence 2912, Appl
17	109.5	4.0	617	4	US-09-134-001C-4012	Sequence 4012, Appl
18	109	4.0	222	4	US-09-134-001C-4748	Sequence 4748, Appl
19	109	4.0	649	4	US-08-800-291B-5	Sequence 5, Appl
20	108	4.0	649	4	US-08-800-291B-6	Sequence 6, Appl
21	107.5	3.9	492	4	US-09-134-001C-4847	Sequence 4847, Appl
22	107	3.9	776	4	US-09-165-396-3	Sequence 3, Appl
23	104.5	3.8	518	4	US-09-134-001C-4744	Sequence 744, Appl
24	103.5	3.8	450	4	US-09-134-001C-4858	Sequence 4858, Appl
25	103	3.8	324	4	US-09-134-001C-5525	Sequence 5525, Appl
26	103	3.8	373	4	US-09-134-001C-4029	Sequence 4029, Appl
27	103	3.8	405	4	US-09-134-001C-4999	Sequence 4999, Appl

ALIGNMENTS

1

RESULT 1	US-09-677-734A-12
GENERAL INFORMATION:	Sequence 12, Application US/08677734A
APPLICANT:	Brant, Steven R.
APPLICANT:	Yun, Chris C.H.
APPLICANT:	Donowitz, Mark
APPLICANT:	Tse, Chung-Ming
TITLE OF INVENTION:	Cloning, Tissue Distribution, and Functional Analysis Of The Human Na+/H+ Exchanger Isoform.
TITLE OF INVENTION:	NHE3.
NUMBER OF SEQUENCES:	12
CORRESPONDENCE ADDRESS:	
ADDRESSEE:	Dunner, Farabow, Garrett & Dunner
STREET:	1300 I Street, N.W., Suite 700
CITY:	Washington
STATE:	D.C.
COUNTRY:	USA
ZIP:	20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/677734A

FILING DATE: 10-JUL-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Fordis, Jean B.

REGISTRATION NUMBER: 32,984

REFERENCE/DOCKET NUMBER: 053387.0043-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 832 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-677734A-12

Query Match Score 491; DB 2; Length 832;
Best Local Similarity 31.7%; Pred. No. 5.4e-39;
Matches 145; Conservative 88; Mismatches 172; Indels 52; Gaps 18;

Qy 25 INLFVALCACIVLGHLEE-NRWVNESITALLIIGCTGVVILLMTKGKSSH--FVFSE 81
 Db 57 IALWVLVASLAKITVPHLSHKTVSVPPSALLIVLGVLGGTVL----AHDIASFTLTP 111
 Qy 82 DLFFYLLPPIFNAGFOVKKKOFFRFMFTITLEGAVGTMMISFTTISIAAAIFSRMNIG 141
 Db 112 TVEFFYLLPPIVDAGFMPPNRLFFNSNLGSILLYAVVGTWNNAATGSLSYGVFLSGIMG 171
 Qy 142 TLDVDG--DFAIGAIFASATDSVCTLQLNQ-DETPFLYSLVGEVVNDATSVLNFNALQ 198
 Db 172 EKIGLDFDLFGLGSIAAVDPAVLAFFEEHVNEVLFITFGESLINDATVVLXNFQ 231
 Qy 199 NFDLVHDAV--VLFKLGNFYFLFSSTFLG-VFAGLSSAYIKLYIGRHSTDREVA 254
 Db 232 SPTVLGSDKVTGVDCKVKGIVSFVVSUGGTLVGVVRAFLIS-LVTR-FTKHVRVTEPG 287
 Qy 255 MMMLMAYLSSYMLAELLDGILTVFFCGIVMSHYTNWNTBSSRVTTKHAFATLSFTAET 314
 Db 288 FVFIISLPSYLTSEMISLSSSLAITCGICCKYKANISSQSATVRYTMKMLASGAET 347
 Qy 315 FLFLYYGMDALD--IEKWEEFASDRPGKSIGSSILGLVGRAAFVPLSFLSNLKKA 372
 Db 348 1TFMFLGISAUDPLINTWNTAFR-----LTLFLFVSYTRAIGCVLQTLWLNRYRMV 398
 Qy 373 PNEKITWROQVVIWAGLMRASVIALAYNFTRSSHTQLQIGNAT---MTISTUTVLF 428
 Db 399 QLELI--DQVMSVYGL--REGAVAFALV-----ALLEGNKYKEKKNLVESTLIVVF 445
 Qy 429 STMVF-GMMTPKLIR-LLLPASGHPVTESSPPSKSLH 463
 Db 446 FTVIQLGLTIKPLVQWLKVKESEH--REPKLNKEKLH 479

RESULT 2
 US-09-097-053-12
 ; Sequence 12, Application US/09097053
 ; Patent No. 6392025
 ; GENERAL INFORMATION:
 ; APPLICANT: Brant, Steven R.
 ; APPLICANT: Yun, Chris C.H.
 ; APPLICANT: Donowitz, Mark
 ; APPLICANT: Tse, Chung-Ming
 ; TITLE OF INVENTION: Cloning, Tissue Distribution, and
 ; Functional Analysis Of The Human Na+/H+ Exchanger Isoform,
 ; TITLE OF INVENTION: NHE3.
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/097,053
 ; FILING DATE:
 ; CLASIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/677,734
 ; FILING DATE: 10-JUL-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Foridis, Jean B.
 ; REGISTRATION NUMBER: 32,984
 ; REFERENCE/DOCKET NUMBER: 05387-0043-00000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 408-4000
 ; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 832 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: Peptide
 ; US-09-097-053-12
 ; Query Match 18.0%; Score 491; DB 4; Length 832;
 ; Best Local Similarity 31.7%; Pred. No. 5.e-39;
 ; Matches 145; Conservative 88; Mismatches 172; Indels 52; Gaps 18;
 Qy 25 INFVALLCACIVLGHLEE-NRWVNESITALLIIGCTGVVILLMTKGKSSH--FVFSE 81
 Db 57 IALWVLVASLAKITVPHLSHKTVSVPPSALLIVLGVLGGTVL----AHDIASFTLTP 111
 Qy 82 DLFFYLLPPIFNAGFOVKKKOFFRFMFTITLEGAVGTMMISFTTISIAAAIFSRMNIG 141
 Db 112 TVEFFYLLPPIVDAGFMPPNRLFFNSNLGSILLYAVVGTWNNAATGSLSYGVFLSGIMG 171
 Qy 142 TLDVDG--DFAIGAIFASATDSVCTLQLNQ-DETPFLYSLVGEVVNDATSVLNFNALQ 198
 Db 172 EKIGLDFDLFGLGSIAAVDPAVLAFFEEHVNEVLFITFGESLINDATVVLXNFQ 231
 Qy 199 NFDLVHDAV--VLFKLGNFYFLFSSTFLG-VFAGLSSAYIKLYIGRHSTDREVA 254
 Db 232 SPTVLGSDKVTGVDCKVKGIVSFVVSUGGTLVGVVRAFLIS-LVTR-FTKHVRVTEPG 287
 Qy 255 MMMLMAYLSSYMLAELLDGILTVFFCGIVMSHYTNWNTBSSRVTTKHAFATLSFTAET 314
 Db 288 FVFIISLPSYLTSEMISLSSSLAITCGICCKYKANISSQSATVRYTMKMLASGAET 347
 Qy 315 FLFLYYGMDALD--IEKWEEFASDRPGKSIGSSILGLVGRAAFVPLSFLSNLKKA 372
 Db 348 1TFMFLGISAUDPLINTWNTAFR-----LTLFLFVSYTRAIGCVLQTLWLNRYRMV 398
 Qy 373 PNEKITWROQVVIWAGLMRASVIALAYNFTRSSHTQLQIGNAT---MTISTUTVLF 428
 Db 399 QLELI--DQVMSVYGL--REGAVAFALV-----ALLEGNKYKEKKNLVESTLIVVF 445
 Qy 429 STMVF-GMMTPKLIR-LLLPASGHPVTESSPPSKSLH 463
 Db 446 FTVIQLGLTIKPLVQWLKVKESEH--REPKLNKEKLH 479

RESULT 3
 US-08-677-734A-9
 ; Sequence 9, Application US/08677734A
 ; Patent No. 5871919
 ; GENERAL INFORMATION:
 ; APPLICANT: Brant, Steven R.
 ; APPLICANT: Yun, Chris C.H.
 ; APPLICANT: Donowitz, Mark
 ; APPLICANT: Tse, Chung-Ming
 ; TITLE OF INVENTION: Cloning, Tissue Distribution, and
 ; Functional Analysis Of The Human Na+/H+ Exchanger Isoform,
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dunner
 ; STREET: 1300 I Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/097,053
 ; FILING DATE:
 ; CLASIFICATION:
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/677,734
 ; FILING DATE: 10-JUL-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Foridis, Jean B.
 ; REGISTRATION NUMBER: 32,984
 ; REFERENCE/DOCKET NUMBER: 05387-0043-00000
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 408-4000
 ; TELEFAX: (202) 408-4400
 ; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/677,734A
 FILING DATE: 10-JUL-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Fordis, Jean B.
 REGISTRATION NUMBER: 32,984
 REFERENCE/DOCKET NUMBER: 05387.0043-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-4000
 TELEFAX: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 834 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-677-734A-9

Query Match 17.7%; Score 482.5; DB 2; Length 834;
 Best Local Similarity 31.4%; Pred. No. 3 6e-38;
 Matches 136; Conservative 88; Mishatches 158; Indels 51; Gaps 17;

QY 48 VNESTITALIIGLCTGVVLLMTKGKSSHL--FVSESDLEFFYLPLPPIFNAGFQYKKQF 105
 Db 82 VPESALLIVLGLVGGIV----WAADHIASTFLTPVFFYLPLPPIVLDAGYFMPNRLF 136

QY 106 FRNEMTILFGAVGTMISFFTTISAAIAIFSRMNIGLTLDVG--DFLAIGAFSATDSVCT 163
 Db 137 FGNIGTLLYAVVGTWNNAATGGVFLSGLMGDLQIGLDFLLFGSLMAAVDPVAV 196

Qy 164 LOYLNQ-DETPFLYSLVGEGLDNLV---HIDAAVVLKFELGSNFY 219
 Db 197 LAYEEVHVNEVLFILVGESELNDATVVILNFSFVALGGDNVTGDCVKGIVSFV 256

Qy 220 LFLSSTFLG-VFAGLSSAYIKKLYIGRHSTDREVALMMLMAYLSYMLAEULLDLSGLITY 278
 Db 257 VSUGGTLLGVVFAPLL--LVTR--FTKHVRITTEPGEFLFISYLSLTSEMSSLSATAI 312

Qy 279 FFGCIVMSHYTWINTESTRVTIKHAPATLSTFAETFLFLYGMDALDIEKWFAASDRPG 338
 Db 313 TFCGICCKORYKVNANEQSATTIVRTYMMIASSAETTIFMELGISAYNPFIWTW---- 366

Qy 339 KSTGIISSILLGLVIG--RAAFVFPPLSLSNLNTKKAPNEKITWROQVVIWAGLMRGAVS 396
 Db 367 ---NTAFVLLTFLISVYRAIGVYQLQWLNNRYRMVQLEPI---DQVVLSYGGL-RGAVA 419

Qy 397 IALLYNKFRSGHTQLHGNAI---MTISTITVVLFSMDFE-GMMTKPLIR-LLPPASH 450
 Db 420 FALV-----VLDGDKVKVEKNLFLVSTT1IVFFVIFQGLTIKPLVQWLKVKRSEH 470

Qy 451 PVTEPSSPKSLH 463
 Db 471 ---REPRNEKLH 480

RESULT 4
 US-08-677-734A-10
 ; Sequence 10, Application US/08677734A
 ; Patent No. 5871919
 ; GENERAL INFORMATION:
 ; APPLICANT: Brant, Steven R.
 ; APPLICANT: Yun, Chris C.H.
 ; APPLICANT: Donowitz, Mark
 ; APPLICANT: Tse, Chung-Ming
 ; TITLE OF INVENTION: Cloning, Tissue Distribution, and
 ; TITLE OF INVENTION: Functional Analysis Of The Human Na⁺/H⁺ Exchanger Isoform,
 ; TITLE OF INVENTION: NHE3.
 ; NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 STREET: 1300 I Street, N.W., Suite 700

RESULT 5
 US-09-097-053-9
 ; Sequence 9, Application US/09097053
 ; Patent No. 6392025
 ; GENERAL INFORMATION:
 ; APPLICANT: Brant, Steven R.
 ; APPLICANT: Yun, Chris C.H.

APPLICANT: Donowitz, Mark
 APPLICANT: Tse, Chung-Ming
 TITLE OF INVENTION: Cloning, Tissue Distribution, and
 Functional Analysis Of The Human Na+/H+ Exchanger Isoform,
 NHE3.
 NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
 ADDRESSEE: Danner
 STREET: 1300 I Street, N.W., Suite 700
 CITY: Washington
 STATE: D.C.
 ZIP: 20005-3315

COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/097,053
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/677,734
 FILING DATE: 10-JUL-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Fordis, Jean B.
 REGISTRATION NUMBER: 32,984
 REFERENCE/DOCKET NUMBER: 05387.0043-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-4000
 TELEX/FAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 834 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-09-097-053-9

Query Match 17.7%; Score 482.5; DB 4; Length 834;
 Best Local Similarity 31.4%; Pred. No. 3.6e-38;
 Matches 136; Conservative 88; Mismatches 158; Indels 51; Gaps 17;

QY 48 VNESTALILGLCTGVILLMTKGSSHL -FVFSEDLFLPPIIFNAFGQVKKKOF 105
 DB 82 VPESALLIVLVLGGIV ---WAADHAASFLTLPVTEFFYLPLPVIDAGYMPNRLF 136

QY 106 FRNFMITLFLGAVGTMISFFTISIAIAIFSRMNIGTLDVG --DFAIAGAIFSATDSVC' 163
 DB 137 FGNLGTLIYAVGVWNAATGTGSLYGLMGLDQIGLDFLLFGSLLMAAVDPYAV 196

QY 164 LOVLNQ -DETPFLYSLVFGEGVVNDATSVLFLNALQNFDLY -- HIDAAYVVLKLGNFYY 219
 DB 197 LAVFEVHVNEVLFIVFGESLLDAVTLYNFEVYALGGDNVNTGYDCVKGIVSFYV 256

QY 220 UFLSSTFLG-VFAGLSSAYIKKLYIGRUSTDREVALMLMAYLSMIAELLDLSGLTY 278
 DB 257 VSLGGTLVSWFAFLS -LVR -FTKHVRIIEPGFVIIIPGMLRQYVLTSEMLSISAIAI 312

QY 279 FFCGTIVMSHYWNVNTTESSRVTTKAHATLFLPVGMDALDEKWEFASDRG 338

DB 313 TFCGICQCQKVAKNISEQATVRYTMNASSSETIIFMFLG-SAVNFITWW---- 366

QY 339 KSIGISSISSLGLVLIG -RAAFYFVPLSFLSNLTKKAPNEKITWQVYVWAGLMRGAVS 396

DB 367 ---NTAFVLLTFLVFSVTRAGVLTWLNTRMVQLEPPI --DQVVLSYGGL-RGAVY 419

QY 397 IALYNKFTRSGHTQLHGNAT ---MITSTITVLFSTMVF -GMMTKPLIR -LLLPAIGH 450

DB 420 FALV-----VLLDDGDKVEKKNLFYSTTLLVVFQGUTKPLVQWLKVKRSEH 470

QY 451 PVTSEPPSPKSLH 463
 Db 471 --REPRLNKEKLH 480

RESULT 6
 US-09-097-053-10
 Sequence 10, Application US/09097053
 Patent No. 639205

GENERAL INFORMATION:
 APPLICANT: Brant, Steven R.
 APPLICANT: Yun, Chris C.H.
 APPLICANT: Donowitz, Mark
 APPLICANT: Tse, Chung-Ming
 TITLE OF INVENTION: Cloning, Tissue Distribution, and
 Functional Analysis Of The Human Na+/H+ Exchanger Isoform,
 NHE3.
 NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &
 ADDRESSEE: Danner
 STREET: 1300 I Street, N.W., Suite 700
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3315

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/097,053
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/677,734
 FILING DATE: 10-JUL-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Fordis, Jean B.
 REGISTRATION NUMBER: 32,984
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 834 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: peptide
 US-09-097-053-10

Query Match 17.7%; Score 482.5; DB 4; Length 834;
 Best Local Similarity 31.4%; Pred. No. 3.6e-38;
 Matches 136; Conservative 88; Mismatches 158; Indels 51; Gaps 17;

QY 48 VNESTALILGLCTGVILLMTKGSSHL -FVFSEDLFLPPIIFNAFGQVKKKOF 105
 DB 82 VPESALLIVLVLGGIV ---WAADHAASFLTLPVTEFFYLPLPVIDAGYMPNRLF 136

QY 106 FRNFMITLFLGAVGTMISFFTISIAIAIFSRMNIGTLDVG --DFAIAGAIFSATDSVC' 163
 DB 137 FGNLGTLIYAVGVWNAATGTGSLYGLMGLDQIGLDFLLFGSLLMAAVDPYAV 196

QY 164 LOVLNQ -DETPFLYSLVFGEGVVNDATSVLFLNALQNFDLY -- HIDAAYVVLKLGNFYY 219
 DB 197 LAVFEVHVNEVLFIVFGESLLDAVTLYNFEVYALGGDNVNTGYDCVKGIVSFYV 256

QY 220 UFLSSTFLG-VFAGLSSAYIKKLYIGRUSTDREVALMLMAYLSMIAELLDLSGLTY 278
 DB 257 VSLGGTLVSWFAFLS -LVR -FTKHVRIIEPGFVIIIPGMLRQYVLTSEMLSISAIAI 312

QY 279 FFCGTIVMSHYWNVNTTESSRVTTKAHATLFLPVGMDALDEKWEFASDRG 338

DB 313 TFCGICQCQKVAKNISEQATVRYTMNASSSETIIFMFLG-SAVNFITWW---- 366

QY 339 KSIGISSISSLGLVLIG -RAAFYFVPLSFLSNLTKKAPNEKITWQVYVWAGLMRGAVS 396

DB 367 ---NTAFVLLTFLVFSVTRAGVLTWLNTRMVQLEPPI --DQVVLSYGGL-RGAVY 419

QY 397 IALYNKFTRSGHTQLHGNAT ---MITSTITVLFSTMVF -GMMTKPLIR -LLLPAIGH 450

DB 420 FALV-----VLLDDGDKVEKKNLFYSTTLLVVFQGUTKPLVQWLKVKRSEH 470

TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 635 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-014-969-11

Query Match 4.8%; Score 130.5; DB 2; Length 635;
Best Local Similarity 19.1%; Pred. No. 0.0041; Mismatches 86; Gaps 25;
Matches 118; Conservative 86; Indels 209; Gaps 25;

QY 3 MEVAAARUAGALYTTSDDYA-----SVSINLFLVALCACCIVIGHLEENIRWWNESITALIJI
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 1 MSVGVSHTSAPLSPTSGNSVGMSFSIMDYYVFVLLVLVSLAIGLYHACRGWGRHVGELL 60

QY 57 IG---LCTGVVILLMTGKS-----SHLFVESEDLFPI-----YLLPPIENAG 97
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 61 MADRKMCCLPVAISLJATFOAVATLRLPSELYRFSTQYFLRCCYFLGLIPAHF--- 117

QY 98 FOYKKKOFERNFMFTITLEGAVGMISFTSTIAIAIFSRNIGTLDVGDELAIGAIFSA 157
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 118 -----IPVFYRHLH- TSAYEYLELR- FNK 139

QY 158 TDSVCTQLQVLNQDETPELFLVFGEGVWNDAATSVLFLHIDAAVFLKFGLNF 217
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 140 TVRC-----GTVPPIFQMYTMGVLYAPSIAI-NAVTFQDFD----- 175

QY 218 FYFLFSSTFLGYFAGLISAYIKKLYIGRHSTDREVALMMLMAYSYMLAEFLDISGLT 277
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 176 L-LWLSVIALRIVCTYTAALGGKAVW---TDVFVTLVNLFLGOLAVITYSAKVGLGR 230

QY 278 VFCFGIVMSHTWHNVTSEYRVT-----TKHAFATSFIAETFLFLYVGMDALDIE 328
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 231 V-----WAVASQHGR1SGFELDPDPFVRTFWTLAFCGGYFMMMSLYGVNQAOQV 279

QY 329 KWEFASDRPGKSIGIS-----SILGLVLIG-----RAAFVFP 361
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 280 R--YLSSSTEKAVALSCYAVFPFQQVSLCVGLIGLYMAYQEPMSIOQAQAPDQFV 337

QY 362 LSFSLNLTKKAPNEKTIWRQOYVIIWAGLMRGAVS-TALAYNKFRSGHTQL----- 412
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 338 LYVMDLKLKGPLP-----LPGLFLACLFSCLSTISAFNSLAVTVMEDLIRPWPFEP 390

QY 413 -HGNAIMITSTIP-----VVLFLSTMVFGMMTTPKLIRLILLPASHHPV 452
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 391 SEARAIMLRSRGLAFGYYGLLGUMAYISSQMGFVQLQAAISTEGMVGSPGLGFCLGMFFPC 450

QY 453 TSBSSPSLHHSPL-----LTSM-----QSDSLSPSTN--TVRPLLRLM 490
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 451 ANPGAVVGLLAGLVMAFWIGIGSTIVSMGFSMPPSPNSGSSFSLPTNLTVATVTLMLP 510

QY 491 LT--KPT-----HTVHYWW 502
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 511 TTSKPKTGQRFYLSYIW 529

RESULT 11
US-09-134-001C-4425
; Sequence 4425, Application US/09134.001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; CURRENT APPLICATION NUMBER: US/09/134,001C
; FILE REFERENCE: GTC-007
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIORITY NUMBER: US 60/055,779
; SEQ ID NO: 5655
; LENGTH: 000
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-5655
; Sequence 5655, Application US/09134.001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; CURRENT APPLICATION NUMBER: US/09/134,001C
; FILE REFERENCE: GTC-007
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-08-14
; PRIORITY NUMBER: US 60/055,779
; SEQ ID NO: 5655
; LENGTH: 000
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis

Query Match 4.4%; Score 118.5; DB 4; Length 800;
Best Local Similarity 21.3%; Pred. No. 0.0085; Mismatches 71; Indels 129; Gaps 22;
Matches 101; Conservative 71; Indels 129; Gaps 22;
Qy 57 IGLCTGVVILLMTKG----KSSHFLVFSEDL--FIFIYLPLIIFNAGFQVKKQFRRNEM 110
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |

Db 79 LSLMFGSLIISLIGVFFFYATQYLHSTDNLPRFFIYLLFMSMIGIVIA-----NNTI 133
 Qy 111 TITLEGAVGTMISFFTIS-----IAATAIFRMNIGTLDGYDFLTAIGAIFSATDSV 161
 Db 134 IMLYFWELTSSESSLISLISYNNNGESQQLAIQSFMITVEGGLALLTGFILYITITGNTI 193
 Qy 162 CTQVLNQDENT-----PFLYSLVLGVNDATSVLNFALQNFDL----- 202
 Db 194 :-----AFTKSAQFPFHILPRAAMAAP 240
 Qy 203 -----WHDAAVVLKFLGNFFYLFSLSSTFLGVFAGLSSAYTIKKLYIGRHSTDREVALMML 258
 Db 241 TPSAVLHSATMVK -AGTFLFLFRTPLL-----GLSNVTTYTFVFG-----LIT 284
 Qy 259 MAYLSYMLAELLDLSGIL-----HVTWHVNTESSRVTKHAFATLS 309
 Db 285 MFLGSITALRQDILKGILAYSTISQLMGIMMTMVGGLGGQAOTSDELSFKYLVLAGLF 344
 Qy 310 FIATEFLF--LYVGMDALDIKEWFAASDRPGKSTG-----ISSILGLGVLIG - 354
 Db 345 HLMNHAVFKCALFGVGLIDHE----SGVDRDTRLNGMRKVFPKMHITVMILAALSMAGYP 400
 Qy 355 -RAAFVPEPLSFLSNTKAPNERITWRCQVVIWAGLMRGAVSTALA-----YN 402
 Db 401 FLNGFLSKEMFLDSLTKANEFLDQIGFVLTFLVIIISIGVVIASILTYALMIKETFGYN 460
 Qy 403 -KEFRSGHTQLHG-----NAIMTITSTVLFSTMVFGMMTPKLIRULLPAS 448
 Db 461 IEKFRRK--QIHEPWLFSLPAVILMLTPVIIIFPVNPVFGNF-----VILPAT 505

RESULT 13
 ; Sequence 3487 Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; PRIORITY NUMBER: 1998-08-13
 ; PRIORITY NUMBER: US 60/064,964
 ; PRIORITY NUMBER: 1997-11-08
 ; PRIORITY NUMBER: US 60/055,779
 ; PRIORITY NUMBER: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO: 3487
 ; LENGTH: 477
 ; TYPE: PRT
 ; ORGANISM: *Staphylococcus epidermidis*

US-09-134-001C-3487
 ; Sequence 3487 Application US/09134001C
 ; Patent No. 6380370
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134,001C
 ; PRIORITY NUMBER: 1998-08-13
 ; PRIORITY NUMBER: US 60/064,964
 ; PRIORITY NUMBER: 1997-11-08
 ; PRIORITY NUMBER: US 60/055,779
 ; PRIORITY NUMBER: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5674
 ; SEQ ID NO: 3487
 ; LENGTH: 477
 ; TYPE: PRT
 ; ORGANISM: *Staphylococcus epidermidis*

Query Match 4.28; Score 114; DB 4; Length 1394;
 Best Local Similarity 21.6%; Pred. No. 0.057;
 Matches 119; Conservative 87; Mismatches 206; Indels 140; Gaps 27;

Qy 10 LGALYTTSYDAYSVVSINFEVALICACTVGHLEENRWVNESTITALIGLCTGVW-----64
 Db 454 LPMCVVT -KSLLCIG-QAGILTAIILQIL-----TESFCVSIILLATVLFITSK 505
 Qy 65 ILMTKGKSSHLFVFSDEL-----FIYLLPPLIFNAGEFOVKKOFFNEMTITP 115
 Db 506 ISISTSEKISSICRISQSIFVTAIAFCNGFDWLNPIA-----IKILLI 549
 Qy 116 GAVGTMISFFTISAAIAIFSRMNI-----GTLDVGDFLTAIGAIFSATDSVCTUOY 166
 Db 550 ---LSLSPLTICITKIHITYLISLNSSGSHVKGSLVFTLFGTFLGVEG-----TINV 599
 Qy 167 LNQDETPLFLSYVFGEGVYNDATSVLFLNQDNFLVHDAAVVLKFVGNFFYFLSSTF 226
 Db 600 IK -----IEILIGFG-----ALCILSNT - NEGLVLRDTCYR - IGRY - -KLMPTF 642
 Qy 227 LGVAGLSSAYIJKKLYIGRHST -DREY - ALMMLMAYSLMIAELDLISGLTIVFRRGI 283
 Db 643 TDLGHG - ASYSLDEEDTSYSEIHERKISSQFOLYKPSMILISLGEMLTIAWGLNV 700
 Qy 284 VMSHYTWINVTESSRVTKHAFAT -----LSFIATBFLFLYVGMDALDIBKEWEFASDRPGKS 340
 Db 701 YLKNLKFH-----LFAFSSVSTFGITSL 234
 Qy 206 DAAVVLKFLGNFFYLELSSSTFLGVFAGLSSAYTIKK-----LYIGRHSTDREV 253
 Db 235 -PVIVTFVLGNTAIIITFTTROUKLKHPLNMVRFNKVFETLSAVSSMILVYTMVS-----288
 Qy 254 ALMMMLMAYSLMIAELDLISGLTIVFRRGI 308
 Db 289 PALLPIYQTGQGOSALLSGV -VVLPGAVINGLT - NYVTGKIFDKIGIKVLYPGF 343
 Qy 309 -SFIAETFLFLYVGMDALDIEKWEFASDRPGKSISLISLGLVJGRAAEFPEPLSLS 366
 Db 344 ILLISITFLYFLSFL-----PTGTPWNVFLVYLTYTIRNIALGLVUMPLNTVGL 388
 Qy 367 NLTKKAPNEKTWRCQVVIWAGLMRGAVS1 - ALAYNKFTRSCHTQ-----LH 413
 Db 389 NALESDDVSHGTAIMNSRLITAGANGTAVSYTILSIVAKYTAASHTMSKMKLTOEATVH 448
 Qy 414 G -NAIMITSTTIVVLFSTWVF 433
 Db 449 GIDVAFIIFTVLILIGFLALF 470

RESULT 14
 US-09-213-053-2
 ; Sequence 2 Application US/09213053
 ; Patent No. 6159477
 ; GENERAL INFORMATION:
 ; APPLICANT: AUDONNET, Jean-Christophe
 ; TITLE OF INVENTION: CANTINE HERPESVIRUS BASED RECOMBINANT LIVE VACCINE, IN
 ; TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, RABIES OR THE
 ; TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS
 ; FILE REFERENCE: 454313-2200
 ; CURRENT APPLICATION NUMBER: US/09/213,053
 ; CURRENT FILING DATE: 1998-12-16
 ; EARLIER APPLICATION NUMBER: 96088242
 ; EARLIER FILING DATE: 1996-06-27
 ; EARLIER APPLICATION NUMBER: PCT/FR97/01115
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 2
 ; LENGTH: 1394
 ; TYPE: PRT
 ; ORGANISM: Canine herpesvirus
 US-09-213-053-2

Query Match 4.28; Score 113; DB 4; Length 1394;
 Best Local Similarity 21.6%; Pred. No. 0.057;
 Matches 119; Conservative 87; Mismatches 206; Indels 140; Gaps 27;

Qy 10 LGALYTTSYDAYSVVSINFEVALICACTVGHLEENRWVNESTITALIGLCTGVW-----64
 Db 454 LPMCVVT -KSLLCIG-QAGILTAIILQIL-----TESFCVSIILLATVLFITSK 505
 Qy 65 ILMTKGKSSHLFVFSDEL-----FIYLLPPLIFNAGEFOVKKOFFNEMTITP 115
 Db 506 ISISTSEKISSICRISQSIFVTAIAFCNGFDWLNPIA-----IKILLI 549
 Qy 116 GAVGTMISFFTISAAIAIFSRMNI-----GTLDVGDFLTAIGAIFSATDSVCTUOY 166
 Db 550 ---LSLSPLTICITKIHITYLISLNSSGSHVKGSLVFTLFGTFLGVEG-----TINV 599
 Qy 167 LNQDETPLFLSYVFGEGVYNDATSVLFLNQDNFLVHDAAVVLKFVGNFFYFLSSTF 226
 Db 600 IK -----IEILIGFG-----ALCILSNT - NEGLVLRDTCYR - IGRY - -KLMPTF 642
 Qy 227 LGVAGLSSAYIJKKLYIGRHST -DREY - ALMMLMAYSLMIAELDLISGLTIVFRRGI 283
 Db 643 TDLGHG - ASYSLDEEDTSYSEIHERKISSQFOLYKPSMILISLGEMLTIAWGLNV 700
 Qy 284 VMSHYTWINVTESSRVTKHAFAT -----LSFIATBFLFLYVGMDALDIBKEWEFASDRPGKS 340
 Db 701 YLKNLKFH-----LFAFSSVSTFGITSL 234
 Qy 206 DAAVVLKFLGNFFYLELSSSTFLGVFAGLSSAYTIKK-----LYIGRHSTDREV 253
 Db 235 -PVIVTFVLGNTAIIITFTTROUKLKHPLNMVRFNKVFETLSAVSSMILVYTMVS-----288
 Qy 254 ALMMMLMAYSLMIAELDLISGLTIVFRRGI 308
 Db 289 PALLPIYQTGQGOSALLSGV -VVLPGAVINGLT - NYVTGKIFDKIGIKVLYPGF 343
 Qy 309 -SFIAETFLFLYVGMDALDIEKWEFASDRPGKSISLISLGLVJGRAAEFPEPLSLS 366
 Db 344 ILLISITFLYFLSFL-----PTGTPWNVFLVYLTYTIRNIALGLVUMPLNTVGL 388
 Qy 367 NLTKKAPNEKTWRCQVVIWAGLMRGAVS1 - ALAYNKFTRSCHTQ-----LH 413
 Db 389 NALESDDVSHGTAIMNSRLITAGANGTAVSYTILSIVAKYTAASHTMSKMKLTOEATVH 448
 Qy 414 G -NAIMITSTTIVVLFSTWVF 433
 Db 449 GIDVAFIIFTVLILIGFLALF 470

Qy 341 IGISSILGLVIGRAAFVFPLSF----LSNLTKKAPNEKITWQQVVIWWAGLMRGA- 394
 Db 741 --ILLICLLEIASLISVLGNFSPPLLTITISLYSLYLRKQT---QGVNRLA 794
 Qy 395 --VSIALAYNKFRSGLTQLHGNAT----MITSTIVVLFSMVFMMTKPLIRLIL 445
 Db 795 TYISRALLIGLYMTGICYIFIKTNMSFKNFYLIVIIIFINSLITSASTSKSTPTEI 854
 Qy 446 PASGHPVTSSEPPSPKSUHSPPLL-TSMQGSDELSTNNIVRPSSTRLMLTKPTHTVHYW 502
 Db 855 P-----TSANESPASIDTTITKPISTEANNLKSVSTSKPKNLKKLLKS----- 900
 Qy 503 RKFDDALMRPMF 514
 Db 901 KCRDNVLYRPF 912

RESULT 15
 US-08-800-291B-4
 ; Sequence 4, Application US/08800291B
 ; Patent No. 6153740

; GENERAL INFORMATION:
 ; APPLICANT: J.D. Young & C.E. Cass
 ; TITLE OF INVENTION: cDNA ENCODING NUCLEOSIDE TRANSPORTER
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 4225 Executive Square, Suite 1400
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/800,291B
 ; FILING DATE: 13-FEB-1997
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/499,314
 ; FILING DATE: 7-JULY-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Haile, Lisa A.
 ; REGISTRATION NUMBER: 38-347
 ; REFERENCE/DOCKET NUMBER: 07254/044WO1
 ; TELEPHONE: 619/678-5070
 ; TELEFAX: 619/678-5099
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 650 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

US-08-800-291B-4

Query Match 4 18; Score 111; DB 4; Length 650;
 Best Local Similarity 21.3%; Pred. No. 0.034;
 Matches 98; Conservative 51; Mismatches 174; Indels 138; Gaps 19;

Qy 21 SVSINFLVALLCAC----IVLGHLEEN----RWNNESTA 54
 Db 182 SFAGICVFVALLFACSKHICAVSRMRAVSNGLGLOFVLGLVIRTEPGFLAFEMIGEQLR- 240

Qy 55 LIIGLCTGVYLLMTKGSSHLFVSE ---DIFTYLLPPIFNAGQVKKKQFFRFNM 110
 Db 241 -----IFLSYTAKGSS--FVFGEAIVKDVFAFQVLPIVFFS-----C 276

Qy 111 TITLFGAVGTMSFFTISIAIAFSRMNIGTLVDGLAIGAFSATDSVCTLQVNQD 170

Db 277 VISLYHGLM---QWYTLKLAWLMOVTMGTTATETLSVAGNF-----VSQT 321
 Qy 171 ETPFL-----YSLVFGE-----GVNDATSVLFNALQNFDL 202
 Db 322 EAPLILRPLADMTLSEYHVVMGGYATAGSLLGAYISFGI--DATLILIANSYM---- 374
 Qy 203 VHDAVVLKFLGNFELFLSSTFLGVPAFLSAYIJKLYIGRHSRDEVALMM---- 257
 Qy 258 -LNAYLSYM-----LAELLDLSGLTVFFCGIV----MSHTWHNVTESSRT 300
 Db 375 ----APCAIALSKVYYPEEESFRREEGVKLTYGDONLIAASTGAAISVVKVANIA 430
 Qy 431 ANLIAFLAVLDEFINALSWLGMVDIOGLSFQLICSYILRPVAFLMGVAEDCPVVAELL 490
 Qy 301 TKHAFTLSEIAETFLFLVYGMDALIEKWEFASDRPGKSIGISSLGLVIGRAAEVF 360
 Db 491 GTKLFLN-EFVAYQDLSKYKORRLAGAEEW- VGDRKQWISVRAEVLTFAI⁺CGEANESS 547
 Qy 361 PLSFSLNTKPKAPNEKRTARQVVTWAGLMRGA-VSTALA 400
 Db 548 IGIMUGGLTSMVPORKSDFSQTVL--RALFTGACVSLVNA 585

Search completed: March 26, 2003, 18:54:54
 Job time : 34 secs

4 protein - protein search, using sw model									
on:	March 26, 2003,	Search time	35 Seconds	(without alignments)					
file:	US-09-888-035A-2								
perfect score:	2722	237916 seqs,	58723674 residues						
sequence:	1 MGMEVAAARLGALYTTSDYA.....GRGFVPPSPGSPTEQSHGGR	535							
scoring table:	BLOSUM62								
Gapop 10.0 , Gapext 0.5									
searched:									
total number of hits satisfying chosen parameters:	237916								
minimum DB seq length:	0								
maximum DB seq length:	2000000000								
post-processing:	Minimum Match 0%								
	Maximum Match 100%								
	Listing first 45 summaries								
database :	Published Applications_AA;*								
	1: /cgcn2_6/ptodata/1/pubbaa/1/pubbaa/1/us08_new_pub.pep;*								
	2: /cgcn2_6/ptodata/1/pubbaa/1/pubbaa/1/pct_new_pub.pep;*								
	3: /cgcn2_6/ptodata/1/pubbaa/1/pubbaa/1/us06_new_pub.pep;*								
	4: /cgcn2_6/ptodata/1/pubbaa/1/pubbaa/1/us06_pubcomb.pep;*								
	5: /cgcn2_6/ptodata/1/pubbaa/1/pubbaa/1/us07_new_pub.pep;*								
	6: /cgcn2_6/ptodata/1/pubbaa/1/pubbaa/1/us07_pubcomb.pep;*								
	7: /cgcn2_6/ptodata/1/pubbaa/1/pubbaa/1/us07_pubcomb.pep;*								
	8: /cgcn2_6/ptodata/1/pubbaa/1/pubbaa/1/us08_new_pub.pep;*								
	9: /cgcn2_6/ptodata/1/pubbaa/1/pubbaa/1/us09_new_pub.pep;*								
	10: /cgcn2_6/ptodata/1/pubbaa/1/pubbaa/1/us09_pubcomb.pep;*								
	11: /cgcn2_6/ptodata/1/pubbaa/1/pubbaa/1/us10_new_pub.pep;*								
	12: /cgcn2_6/ptodata/1/pubbaa/1/pubbaa/1/us60_new_pub.pep;*								
	13: /cgcn2_6/ptodata/1/pubbaa/1/pubbaa/1/us60_pubcomb.pep;*								
	14: /cgcn2_6/ptodata/1/pubbaa/1/pubbaa/1/us60_pubcomb.pep;*								
Pred.	No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
		SUMMARIES							
		8	Query No.	Match Score	Length Length DB	ID	Description		
1	2082	76.5	546	9	US-10-155-535-2		Sequence 2, Appli		
2	2023.5	74.3	538	9	US-09-834-998A-1		Sequence 1, Appli		
3	1931	70.9	552	9	US-10-155-535-4		Sequence 4, Appli		
4	561	20.6	521	9	US-10-155-535-6		Sequence 6, Appli		
5	545.5	20.0	446	9	US-10-217-096-4		Sequence 4, Appli		
6	541.5	19.9	509	10	US-09-800-729-93		Sequence 93, Appli		
7	541.5	19.9	526	10	US-09-800-729-180		Sequence 180, Appli		
8	539	19.8	645	9	US-10-217-096-2		Sequence 2, Appli		
9	538	19.8	669	9	US-09-834-998A-2		Sequence 2, Appli		
10	533	19.6	633	9	US-09-834-998A-3		Sequence 3, Appli		
11	485	17.8	896	9	US-10-217-096-6		Sequence 6, Appli		
12	478	17.6	822	10	US-09-824-734-3		Sequence 2, Appli		
13	314	17.5	370	10	US-09-800-729-215		Sequence 215, Appli		
14	292.5	10.7	339	10	US-09-800-729-128		Sequence 128, Appli		
15	292.5	10.5	339	10	US-09-800-729-129		Sequence 129, Appli		
16	285.5	10.5	1146	10	US-09-824-734-2		Sequence 2, Appli		
17	231.5	8.5	684	10	US-09-815-242-10712		Sequence 10712, Appli		
18	210	7.1	94	9	US-10-217-096-5		Sequence 5, Appli		
19	192	7.1	94	9	US-10-217-096-4		Sequence 4, Appli		
20	184.5	6.8	686	10	US-09-815-242-5777		Sequence 5777, Appli		
21	184.5	6.8	692	10	US-09-815-242-12734		Sequence 12734, Appli		
22	153.5	5.6	516	9	US-09-738-626-5086		Sequence 5086, Appli		
23	133	4.9	129	9	US-09-925-299-1210		Sequence 1210, Appli		
24	133	4.9	129	10	US-09-925-299-1210		Sequence 9210, Appli		
25	116.5	4.3	480	9	US-09-895-913K-92		Sequence 921, Appli		
26	110.5	4.1	450	10	US-09-741-669-385		Sequence 385, Appli		
27	109.5	4.0	296	10	US-09-815-242-5098		Sequence 5098, Appli		
28	108	4.0	539	10	US-09-815-242-5139		Sequence 5139, Appli		
29	105.5	3.9	461	10	US-09-815-242-12175		Sequence 12175, Appli		
30	105.5	3.9	490	9	US-09-738-626-5881		Sequence 5881, Appli		
31	105	3.9	422	10	US-09-915-242-5682		Sequence 5682, Appli		
32	105	3.9	458	9	US-09-738-626-3886		Sequence 3886, Appli		
33	104	3.8	444	9	US-09-738-626-5577		Sequence 5577, Appli		
34	104	3.8	816	9	US-09-255-088-5		Sequence 5, Appli		
35	103.5	3.8	388	10	US-09-815-242-1458		Sequence 1458, Appli		
36	103.5	3.8	388	10	US-09-881-752A-350		Sequence 350, Appli		
37	102	3.7	494	12	US-10-033-109-6		Sequence 6, Appli		
38	99.5	3.7	717	9	US-09-883-43A-5		Sequence 5, Appli		
39	99.5	3.7	1042	10	US-09-888-615-74		Sequence 74, Appli		
40	99	3.6	371	9	US-09-759-130B-281		Sequence 281, Appli		
41	99	3.6	525	9	US-09-882-694-8		Sequence 8, Appli		
42	99	3.6	962	9	US-09-738-26-3800		Sequence 3800, Appli		
43	99	3.6	1116	9	US-09-835-976B-12		Sequence 12, Appli		
44	97	3.6	497	10	US-09-734-676-2		Sequence 2, Appli		
45	97	3.6	807	10	US-09-895-686-6		Sequence 6, Appli		
ALIGNMENTS									
RESULT 1									
US-10-155-535-2									
; Sequence 2, Application US-10155535									
; Publication No. US20030046729A1									
; GENERAL INFORMATION;									
; APPLICANT: Blumwald, Eduardo									
; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY VACUOLAR CATION-PROTON ANTIPORTERS									
; FILE REFERENCE: 529152000720									
; CURRENT APPLICATION NUMBER: US10/155,535									
; CURRENT FILING DATE: 2002-05-24									
; PRIORITY APPLICATION NUMBER: 09/271,584									
; PRIORITY FILING DATE: 1999-03-18									
; PRIORITY APPLICATION NUMBER: 60/078,474									
; PRIORITY FILING DATE: 1998-03-18									
; NUMBER OF SEQ ID NOS: 27									
; SOFTWARE: FastSEQ for Windows Version 4.0									
; SEQ ID NO: 2									
; LENGTH: 546									
; ORGANISM: Arabidopsis thaliana									
US-10-155-535-2									
Query Match	76.5%	Score 2082;	DB 9;	Length 546;					
Best Local Similarity	76.6%	Pred. No. 7.	8-175;						
Matches 402,	Conservative	54;	Mismatches 61;	Indels 8;	Gaps 2				
Qy	15	TISDYASVINSFLVALCIVLGHLEENRWNESTALIIGLCTGWTLLMTKGKSS	74						
Db	15	STSDHVASVSLNLFVALCACIVLGHLEENRWNESTALIIGLCTGWTLLMTKGKSS	74						
Qy	75	HLPVSEDFYLPLPDIENFGQVKKQFERNFTITLEGAVGTMSEFTTIAAI	134						
Db	75	HLPVSEDFYLPLPDIENFGQVKKQFERNFTITLEGAVGTMSEFTTIAAI	134						
Qy	135	FSRMNIGLTLDYGDFLAIGAIFSATDSVCLQLNQDETFLPFLSYLVGEGVNDATSVLFL	194						
Db	135	FKKDJGTFDGDGLAIGAIFRATDSVCLQLNQDETFLPFLSYLVGEGVNDATSVLFL	194						

Qy 195 NALONFDLVHIDAAVVLKFLGNFFYLFLSSTFLGVFAGLLSAYIJKLYIGRHSTDREVA 254
 Db 195 NATOSFDLTHLNHEAAFQPGNPFYLFLSTGLGVATGILSAYVKKYIGRHSTDREVA 254
 Qy 255 LMMMLMAYLSYMLAELDLSSLGTVFFCGLIVMSHTWHNTESSRVTKHAFATSLFIAET 314
 Db 255 LMMMLMAYLSYMLAELFLASLGTLTVEFFCGLIVMSHTWHNTESSRITKHAFATSLFIAET 314
 Qy 315 FFLFVGMDALDIEKWEFASDRPGKSIGTSISLLGLVIGRAAFVPLSFLSNLKTPN 374
 Db 315 FFLFVGMDALDIEKWEFASDRPGKSIGTSISLLGLVIGRAAFVPLSFLSNLKTPN 374
 Qy 375 EKTTWROQVVIWAGLMGAVSIALTAYNKTRSGHTOLHGNAIMTSTTIVVLFSSTAVFG 434
 Db 375 EKTTWROQVVIWAGLMGAVSIALTAYNKTRSGHTOLHGNAIMTSTTIVVLFSSTAVFG 434
 Qy 435 MMTPKLPIRLLP-----ASGHPTVSEPPSSPKSLSPLTSMQGSDLE--STTINVRPSS 486
 Db 435 MMTPKLPIRLLP-----ASGHPTVSEPPSSPKSLSPLTSMQGSDLE--STTINVRPSS 486
 Qy 487 LRMLLTKTHTHYWYRKFDALMRPMGGFGRGPVFPSPTEQS 531
 Db 495 LRGFLMRPRTRYHYWWQDFDAFMRPVFGGRGPVFPSPTEQS 531
 Qy US-09-834-998A-1 ;
 Db US-09-834-998A-1 ;
 Qy ; Sequence 1; Application US/09834998A
 Db ; Patent No. US20020178464A1
 Qy ; GENERAL INFORMATION:
 Db ; APPLICANT: Gaxiola, Roberto A.
 Qy ; ATTORNEY: Fink, Gerald R.
 Db ; TITLE OF INVENTION: Proton Transporters And Uses In Plants
 Qy ; FILE REFERENCE: 0319-2004-002
 Db ; CURRENT APPLICATION NUMBER: US/09/834,998A
 Qy ; CURRENT FILING DATE: 2001-04-13
 Db ; PRIOR APPLICATION NUMBER: US 09/644,039
 Qy ; PRIOR FILING DATE: 2000-08-22
 Db ; PRIOR APPLICATION NUMBER: US 60/164,808
 Qy ; PRIOR FILING DATE: 1999-11-10
 Db ; SOFTWARE: Fast-SEQ for Windows Version 4.0
 Qy ; SEQ ID NO: 1
 Db ; LENGTH: 538
 Qy ; TYPE: PPT
 Db ; ORGANISM: Artificial Sequence
 Qy ; FEATURE: AtNhxA
 Db ; OTHER INFORMATION: Arabidopsis - AtNhxA
 Qy US-09-834-998A-1 ;
 Qy ; Query Match Score 2023.5; DB 9; Length 538;
 Db ; Best Local Similarity 73.3%; Pred. No. 1.1e-169;
 Qy ; Matches 389; Conservative 60; Mismatches 79; Indels 3; Gaps 2;
 Qy 3 MEVAARLGLAYTTSDYASVVSINLFEALLCIVGHLEENPKVNESTITALIGLC 62
 Db 2 DDSLVRKLPSS-STDSHASYLVAFLVALCIVGHLEENPKVNESTITALIGLC 62
 Qy 123 SFTTISIAAIAIFSRMINTLUDGDFLAIAGAIFSATSDSYCTLOVNQDETPELYSLVGE 182
 Db 121 SCTTISLGVTQFFKLDIGTFDGLDYLATGIAFAATDSVCLQVNQDETPELYSLVGE 180
 Qy 183 GVNDNTSIVLNFNALONFLVHTDAAVVLKFLGNFYLFLSTFLGVFAGLLSAYIKKL 242
 Db 181 GVNDNTSIVLNFNALONFLVHTDAAVVLKFLGNFYLFLSTFLGVFAGLLSAYIKKL 240
 Qy 243 YIGRHSTDREVAMMLMAYLSYMLAELLDISGILTFFCGIUMSHYTWHNTESSRVTK 302
 Db 302 TKHTPAAMSFLAEIIFTYVGMDALDIEKWFALIYQSFEDVFLNAAFHILGFLGAATGISAIVK 360
 Qy 301 TKHAFATLSEFAETEFLYVINGMDALDIEKWFALIYQSFEDVFLNAAFHILGFLGAATGISAIVK 360
 Db 241 YGRRHSTDREVAMMLMAYLSYMLAELLDISGILTFFCGIUMSHYTWHNTESSRVTK 300
 Qy 303 HAETATLSEFAETEFLYVINGMDALDIEKWFALIYQSFEDVFLNAAFHILGFLGAATGISAIVK 362
 Db 301 HTFATLSEFAETEFLYVNGMDALDIEKWFALIYQSFEDVFLNAAFHILGFLGAATGISAIVK 360
 Qy 363 SFSLNLTKKAPNEKTTWROQVVIWAGLMGAVSIALTAYNKTRSGHTOLHGNAIMTST 422
 Db 361 SFSLNLAKKQNQESETINFNMQVVIWAGLMGAVSIALTAYNKTRSGHTOLHGNAIMTST 420
 Qy 423 ITVVLFSTMVFGMTKPLTRLLPASGHVET - SEPPSPSKLSPLTSMOGSDELTNN 480
 Db 421 ITVCLFSITVVFGMITKPLASYLPHONATTSMLSDDNPSPKSIPLLDODSFTEPSGNHN 480
 Qy 481 TVRSSLRMLLKPTHTHYWYRKFDALMRPMGGFGRGPVFPSPTEQS 531
 Db 481 VPRDSDIRGFLLTRTRVHYWWQDFDSFMRPVFGGRGPVFPVGSPSTERN 531
 RESULT 3 ;
 Db US-10-155-535-4 ;
 Qy Sequence 4; Application US/10115535 ;
 Db ; Publication No. US2003046729A1
 Qy ; GENERAL INFORMATION:
 Db ; APPLICANT: Blumwald, Eduardo
 Qy ; ATTORNEY: Apse, Mari
 Db ; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY
 Qy ; EXPRESSION OF VACUOLAR CATION PROTON ANTIPORTERS
 Db ; FILE REFERENCE: 529152000720
 Qy ; CURRENT APPLICATION NUMBER: US/10/155,535
 Db ; CURRENT FILING DATE: 2002-05-24
 Qy ; PRIOR APPLICATION NUMBER: 09/271,584
 Db ; PRIOR FILING DATE: 1999-03-18
 Qy ; PRIOR APPLICATION NUMBER: 60/078,474
 Db ; PRIOR FILING DATE: 1998-03-18
 Qy ; PRIOR APPLICATION NUMBER: 60/116,111
 Db ; PRIOR FILING DATE: 1999-01-15
 Qy ; NUMBER OF SEQ ID NOS: 27
 Db ; SOFTWARE: Fast-SEQ for Windows Version 4.0
 Qy ; SEQ ID NO: 4
 Db ; LENGTH: 552
 Qy ; TYPE: PPT
 Db ; ORGANISM: Arabidopsis thaliana
 Qy US-10-155-535-4 ;
 Qy ; Query Match Score 1931; DB 9; Length 552;
 Db ; Best Local Similarity 69.6%; Pred. No. 1.5e-161;
 Qy ; Matches 377; Conservative 67; Mismatches 78; Indels 20; Gaps 4;
 Qy 1 MGMEVAARLGLAYTTSDYASVVSINLFEALLCIVGHLEENPKVNESTITALIGLC 60
 Db 3 IGLSTMKEATLPE -ADHASVVSNNFIVALIACIVLGHLEETRMNESITALIGLC 61
 Qy 61 TGVVILLMLTKGKSSHLEFEVSEDLFFTYLLPLTFNAQFOVKKQFFENFMITLFGAVGT 120
 Db 62 TGVVILLMLTKGKSSHLEFEVSEDLFFTYLLPLTFNAQFOVKKQFFENFMITLFGAVGT 121
 Qy 121 MISFFPTISIAATPSRNPMLGILDVEFLAIGATFSDVCTLOVNQDETPELYSLV 180
 Db 122 LISFVVISGAKHLFEKMNIGDTIADYLAIGAIFSATDSVCTLOVNQDETPELYSLV 181
 Qy 181 GEGVNDNTSIVLNFNALONFLVHTDAAVVLKFLGNFYLFLSTFLGVFAGLLSAYIK 240
 Db 182 GEGVNDNTSIVLNFNALONFLVHTDAAVVLKFLGNFYLFLSTFLGVFAGLLSAYIK 241
 Qy 241 KLYIGRHSTDREVAMMLMAYLSYMLAELLDISGILTFFCGIUMSHYTWHNTESSRVT 300
 Db 242 KLYIGRHSTDREVAMMLMAYLSYMLAELLDISGILTFFCGIUMSHYTWHNTESSRVT 301
 Qy 301 TKHAFATLSEFAETEFLYVINGMDALDIEKWFALIYQSFEDVFLNAAFHILGFLGAATGISAIVK 360
 Db 302 TKHTPAAMSFLAEIIFTYVGMDALDIEKWFALIYQSFEDVFLNAAFHILGFLGAATGISAIVK 361

Qy 361 PLSFLSNLTKKAPNEKITWROQVYIWWAGLMLRGAVSIALAYNKFRSGHTOLHGNAIMT 4.20
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 362 PLSFLSNLTKKAPNEKITWROQVYIWWAGLMLRGAVSIALAYNQFTSGTTRGVGNAIMT 4.21
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Qy 4.21 STITVVLFSTIMVFGMMTCKPLJIRLLPASCHPVTS-----EPSSPKSLHSPVTS 4.69
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 4.22 STITVVLFSTVFGLITKLVKHLOPSKKSOSATLQLTFLRSSHFDP---ILHEPLIST 4.77
 |||:|||:|||:
 Qy 4.70 MGSDELSTINIVRPSLMLTKEWYKWKFDALMRPMFGGROFVPSGPSPTE 5.29
 |||:|||:
 Db 4.78 QGQEYDPEQHV---SFREWKSPDSRAUTHYWKRFDNAMVRRTGGRvSPVPGSPTE 5.33
 |||:|||:
 Qy 530 QS 531
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 Db 534 NS 535
 ;
 RESULT 4
 ; Sequence 6, Application US/10155535
 ; Publication No. US20030046729A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Blumwald, Eduard
 ; APPLICANT: Apse, Mari
 ; TITLE OF INVENTION: INCREASING SALT TOLERANCE IN PLANTS BY
 ; EXPRESSION OF VACUOLAR CATION-PROTON ANTIPORTERS
 ; FILE REFERENCE: 529152000720
 ; CURRENT APPLICATION NUMBER: US/10/155,535
 ; CURRENT FILING DATE: 2002-05-24
 ; PRIOR APPLICATION NUMBER: 09/271,584
 ; PRIOR FILING DATE: 1999-03-18
 ; PRIOR APPLICATION NUMBER: 60/078,474
 ; PRIOR FILING DATE: 1998-03-18
 ; PRIOR APPLICATION NUMBER: 60/116,111
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 521
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-155-535-6

Query Match 20.6%; Score 561; DB 9; Length 521;
 Best Local Similarity 32.5%; Pred. No. 3_1e-4; Mismatches 205; Indels 68; Gaps 22;

Qy 20 ASVSYINFVALICACIVLGHLEENR-WVNESTITALIGGLCTGYVILLM-TKGKSSH 76
 |||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 22 AAGVGLLQIMMLVLSPFLQFLLPPIQSGESLQFNSGEGHFFMVVI----VASVTGG 134
 |||:
 Qy 77 FVSEDFLFLPPIFNAGFOVKKKQFRNFMITLEGAVGTMISFTTISIAAFATFS 13.6
 |||:
 Db 82 FNPHEEFFFLPFLPPIQSGESLQFNSGEGHFFMVVI----VASVTGG 134
 |||:
 Qy 137 RMNTG-----TLDVGFELAIGAFSTSDVCTLQVLNQDETTP-LYSVFGEGVWDA 188
 |||:
 Db 135 LVIIGGSMYLMYKLFPVCLMGALISATDPVTLVSLFQDYGTDVNLVLYVFGESVINDA 194
 |||:
 Qy 189 TSIVLFNAL---QNFPLVHDAAVYLKFGLNNFFYLFLSSFLGFLVAGLSSLSSAYIJKLY 24.3
 |||:
 Db 195 MATSLYRMTSLVNQSSSGEHHFMVVI----RFFETTAGMSAGVGFTSALLFK-Y 247
 |||:
 Qy 244 TG---RHSDREVALMINMAYMSYMLAFLDLSGLITVFCG1VMSHYTWINTVTESSRV 300
 |||:
 Db 248 AGLDTENQNLCFLPFLPPIQSGESLQFNSGEGHFFMVVI----VGFILSFLFIGVARAV 307
 |||:
 Qy 301 TKHAFATLSPFIAETFLFLVYGM ALDEKWEFASDRGKSIGISSLGLVLIG--RAA 357
 |||:
 Db 308 VSSSFHLSSLAETFTYMGFDIAEQHSWSH-----VGFILSFLFIGVARAV 357
 |||:
 Qy 358 FVFPLSLFSNLTKKAPNEKITWROQVVIWWAGLMLRGAVSIALAYNKF-TRESGHTQLHGN 4.15
 |||:
 RESULT 5
 US-10-217-096-4
 ; Sequence 4, Application US/10217096
 ; Publication No. US2003004933A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Curtis, Rory A.J.; Ferriera, Holly M.
 ; TITLE OF INVENTION: 96895, A Human Sodium-Hydrogen Exchanger
 ; FAMILY MEMBER AND USES THEREFOR
 ; FILE REFERENCE: MPI01-14791RM
 ; CURRENT APPLICATION NUMBER: US/10/217,096
 ; CURRENT FILING DATE: 2002-08-12
 ; PRIOR APPLICATION NUMBER: 60/312,544
 ; PRIOR FILING DATE: 2001-08-15
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 446
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Consensus
 ; US-10-217-096-4

Query Match 20.0%; Score 545.5; DB 9; Length 446;
 Best Local Similarity 34.2%; Pred. No. 5.8e-40;
 Matches 157; Conservative 79; Mismatches 162; Indels 61; Gaps 15;

Qy 27 LFVALUCACTVLGHLEE-NRWVNNESTITALIGGLCTGYVILLMTRGKSHLFLVFSEDLFF 85
 |||:
 Db 4 LIIILVLAKTLAHFLKRLGKAIPPSLMLLAGLGLPIGL-----GLIVLDSEVFF 55
 |||:
 Qy 86 IYLLPPLIFNAGFOVKKKQFRNFMITLEGAVGTMISFTTISIAAFATFS 14.1
 |||:
 Db 56 EILIPPLTFEAGLEDLRLFRNLGTSILLAVLGFLSILAVGFLGFLVPLFGQOLV 115
 |||:
 Qy 14.2 TLVDGDFLTAIGAIFSATDSVCTLQVLNQDE----TFLFLYSLVFGEGVWDASTIVLFNAL 197
 |||:
 Db 116 DDLAAALLFGATLSATDPAVLAKFLKGELKRYNKLGLTFLGSESSLNDAVVLLAVL 175
 |||:
 Qy 198 QNF-----DLVHIDAVVLFRLPNFYLFLSFL-----LI 224
 |||:
 Db 176 ISFAQGDNSEAVEADIFSGVILSFL---VVFEGLLIGLVLGPFLS-----LI 224
 |||:
 Qy 245 GRHSTD-----EVALMMLMAYMSYMLAFLDLSGLITVFCG1VMSHYTWINTVTESSRV 295
 |||:
 Db 225 TRFDDEGPLEDRLTEPLLVLAYLIAEMLGSLGILAVFAGLALSNAVAYANISE 284
 |||:
 Qy 296 SSRVTKHAFATLSPFIAETFLFLVYGM-MDALDIKEWFASTDPRGKSIGISTLGLVY- 351
 |||:
 Db 285 KSRTRYKFWMLSPFEPFLVFLGLSLDSVLWNWANIEDL-BESTVIAFLILAVAI 343
 |||:
 Qy 352 LIGRAAFVFPFLPSLNLTKKAP----NEKLTWROQVVIWAGLARGAVSIALAYN-KFT 405
 |||:
 Db 344 LIARAGVFLLTLLAFLERREKRSNVEHTFDRDVLVWGGLURGAVALALAISGPLT 403
 |||:
 Qy 406 RSGHTOLHGNAIMTSTVFLSTMFVGMNTKPLIRL 4.44
 |||:
 Db 404 LEDTSGSPARDLITLTAVVVLVTVQGITLKPLVYKL 442
 |||:
 RESULT 6
 US-09-800-729-93

; Sequence 93, Application US/09800729
; Patent No. US2002008319A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; PRIORITY APPLICATION NUMBER: PCT/US00/26013
; PRIORITY FILING DATE: 2000-09-22
; PRIORITY APPLICATION NUMBER: 60/155,709
; PRIORITY FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 93
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (20)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (168)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (198)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; LOCATION: (199)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (244)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; LOCATION: (246)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (294)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (294)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (301)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (303)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (493)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (498)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (499)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (505)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-800-729-33

Query Match 19.9% Score 541.5; DB 10; Length 509;
Best Local Similarity 30.8%; Pred. No. 1.5e-39;
Matches 149; Conservative 81; Mismatches 173; Indels 81; Gaps 14;

QY 23 VSINLFVALLCAGTIVLGHILEEN--RWYNESTITALIGLCTGVILL--MTIGKSSHL- 76
Db 19 VXLFLFLLTILITLTIWFLKRRVRFHETGLAMIYGLIVLRLRYGTPATSGRDKSLS 78
QY 77 -----
-----FVFSESDLFFIYLIPPI 92

Db 79 CTQEDRAFDSTLYNVSGKRFEEYLKGEISPGKINSVEONDMLRKVTPEPFVNILLPPI 138
QY 93 IFNAGFQVKKKQFRNEMTITLGAVGTMISFFTISIAIAIFSRMNI-GTLD---VGD 147

; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; PRIORITY APPLICATION NUMBER: PCT/US00/26013
; PRIORITY FILING DATE: 2000-09-22
; PRIORITY APPLICATION NUMBER: 60/155,709
; PRIORITY FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 93
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (20)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (168)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (198)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (199)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (244)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (246)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (294)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (294)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (301)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (303)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (493)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (498)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (499)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (505)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-800-729-180

RESULT 7
US-09-800-729-180
; Sequence 180, Application US/09800729
; Patent No. US2002008319A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; PRIORITY APPLICATION NUMBER: PCT/US00/26013
; PRIORITY FILING DATE: 2000-09-22
; PRIORITY APPLICATION NUMBER: PCT/US00/26013
; PRIORITY FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 180
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (37)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (185)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (215)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (216)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (263)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (311)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (318)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE
; LOCATION: (320)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (510)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (515)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (516)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (522)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-800-729-180

Query Match 19.9%; Score 541.5; DB 10; Length 526;
Best Local Similarity 30.8%; Pred. No. 1.6e-39;
Matches 149; Conservative 81; Mismatches 173; Indels 81; Gaps 14;

Qy 23 VSTINLFVALLCAGTIVLHILEEN--RWVNESTITALLIGCTGVILL--MTKGKSSHLL- 76
Db 36 VXLTFILLTUTLTIWFLKRRLVRYGTVLGLMYLVGLTGTATRGRDKSLS 95

Qy 77 -----FVFSIDLFFTYLPLPI 92
Db 96 CTDQEDRAESTLLVNSGKPFPEYLTKBISPGKINSVEQNQMDLRKVTFDPEYFFNNILLPPI 155

Qy 93 IFNAGFQKKKKQFERNMETITLFGAYCTMISFETISTIAIAIFSRMNI-GTLD---VGD 147
Db 156 IFHAGYSLLKKRFEFRNLGSILAYAFLCTAXSCFIIIGNLYGVVKLMKIMGOLSDFKYYTX 215

Qy 148 FLAIGAFISATDSVCTLOVLNODETP-LYSLVFGCVNDATSTVLFNALQNFDLVHI- 205
Db 216 XLEFGAAISATDPVTILAIFNEHLADYDLYALFGESVNLNAVATLXSSIVAYQAGLN 275

Qy 206 ---DAAVTLKFLGNFYLFLSFLSTLGFAAGLSSATIJKLYIGRHSTD-REVALMLMA 260
Db 276 THAFAAFFPKSVGIFLQIFSSGFTMCAGTVGVTAXTK- FTKXIXXPPLTEALEFLMS 333

Qy 261 YLSYMLAEFLDLGSIGLTVFFCGIVMSHYTWHNVTESSRVITKHAFATLSEIAETFLFLYV 320
Db 334 WSTFLLAEACGFGTVVAFLCGTQAHHTYNNLVSRSRFLAENFITSYM 393

Qy 321 GMDALDIKEWFAASDRPGKSIGISSLGLVJGRAAFYFPEFLSFLSNTKAPNECITWR 380
Db 394 GLAFLTFQRHVFS---PFIIG ---AFVAIFGRAAHAYHPSFLFLNGRR --HKIGWN 443

Qy 381 QQQVVIWAGLMRGAVisIAlAYNKFTRSQHQLHGNATMITSSTTVVLFSTMVFGMMTKPL 440
Db 444 FOHMMEFSSL -RGAMAFAFLAIR-----DTASYARQMMFTTLLIVFFTVWIGGGTTPM 496

RESULT 9
US-09-834-998A-2

Sequence 2, Application US/09834998A
; Sequence 2, Application US/09834998A
; Patent No. US2002018464A1
; GENERAL INFORMATION:
; APPLICANT: Gaxiola, Roberto A.
; ATTORNEY: Fink, Gerald R.
; APPLICANT: Alper, Seth L.
; TITLE OF INVENTION: Proton Transporters And Uses In Plants
; FILE REFERENCE: 0399-2004-002
; CURRENT APPLICATION NUMBER: US/09/834_998A
; CURRENT FILING DATE: 2001-04-13
; PRIORITY NUMBER: US 09/644,039
; PRIOR FILING DATE: 2000-08-22
; PRIORITY NUMBER: US 60/164,808
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 669
; TYPE: PRT
; ORGANISM: Artificial Sequence

RESULT 8
US-10-217-096-2
; Sequence 2, Application US/10217096
; Publication No. US20030044933A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, Rory A.J., Ferriera, Holly M.
; TITLE OF INVENTION: 96895, A Human Sodium-Hydrogen Exchanger
; FAMILY MEMBER AND USES THEREFOR
; FILE REFERENCE: MPI01-147.PRM
; CURRENT APPLICATION NUMBER: US/10/217,096
; CURRENT FILING DATE: 2002-08-12
; PRIORITY NUMBER: 60/312,544
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0

;

FEATURE: ; OTHER INFORMATION: Human - hsNhe-6

Query Match 19.8%; Score 538; DB 9; Length 669;
Best Local Similarity 29.9%; Pred. No. 4.3e-39;
Matches 164; Conservative 97; Mismatches 210; Indels 78; Gaps 18;

QY 1 MGEVAAARLGAALTTSDAYSVSINLEVALLCACIVLGHLLBEN - -RWNESITALLIG
Db 53 MDEEIVSEKQAEEFSHRSANLL--ITFLILITLTITIWFKHARRFLHETGLAMIY 109

QY 59 LCTGVV - - - - -ILLMTKGKSSH --LFVSEDFIYLPLPPIENAGFOVKK 102

Db 110 LLVGLVLHYGIVHPDSVNNVTISCEVOSSPPLLVTDFPEFFNLLPPIFYAGVSLKR 169

Qy 103 KOFFRNEMFTTLEFGAYTMISFFTISTAAIAFESRMNIGTLDVDF----LAIGAIFSA 157

Db 170 RHFTRNLGSILAYAFLGTAISCFVIGSIMYGVTLMKVTGCOLLAGDFYFTDCILFGAIVSA 229

Qy 158 TDSVCTLQLNQDETPE-LYSVFGCVVNDATSIVLNA,ONF ---DLVH- IDAVVL 211

Db 230 TDPVTVAIAFHQLQDVELYALFQGDSVNLNAIVLSSVIVAYQPGDNTSHEDVYTA 289

Qy 212 KFLGNFYLPLPSSTFQGVLSAYI-KLYGRHSTREVALMLMAYLSYMAEL 269

Db 290 RSIGTFGIFSGSFANGAATGVTALEYTKFLK--REFQILLETGLFLFMSWSTFLAEA 346

Qy 270 LDLSGLTUVFCGIVASHYTHWNTESSRTVTKHAFATLSPTAETFLFLYGMDALDIEK 329

Db 347 WGETGVVAVLFCGITOAHYTNINLSTESQHRTKQLEFLNLAENEFSYNGLTLETFQN 406

Qy 330 WEFASDRPGKSIGGISSLLGLIGRAAFVPLSFLSNLTKAPNEKITWROQVVIWAG 389

Db 407 HVF---NPTFVG---AFVAFIFLGRANNIYPLSLLNIGRS--KIGSNEQHNMFMAG 456

Qy 390 LMRGAVSYIALAYNKFRTRSGHTQHGNAIMITSTIVLFLSTMFVGMMTKPLLRLPLPASG 449

Db 457 L-RGAMAFALAR-----DIATYARQMMSTTLLIVEFTWVFGGGTTAMLSCL----- 504

Qy 450 HPTVSEPPSPSLHSPLLTSMQGSDLESTNTIVRSSLRMLLTKPHVYWRKFDDAL 509

Db 505 HIRVGDSDOFHHLGVP-----ENERRTKAESAFLFRM-----WYNFDHNY 545

Qy 510 MRPMFGRG 518

Db 546 LKPPLTHSG 554

RESULT 11
US-09-834-998A-3
; Sequence 3, Application US/09834998A
; Patent No. US2002017844A1
; GENERAL INFORMATION:
; APPLICANT: Gaxiola, Roberto A.
; APPLICANT: Fink, Gerald R.
; APPLICANT: Alper, Seth L.
; TITLE OF INVENTION: Proton Transporters And Uses In Plants
; FILE REFERENCE: 0399 2004-002
; CURRENT APPLICATION NUMBER: US/09/834,998A
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 09/644,039
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/164,808
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Yeast - ScNhx1

US-09-834-998A-3
; Query Match 19.6%; Score 533; DB 9; Length 633;
; Best Local Similarity 26.2%; Pred. No. 1.2e-38;
; Matches 153; Conservative 127; Mismatches 190; Indels 114; Gaps 20;

Qy 16 TSDYASVVSINLEVALLCACIVLGHLLBEN - -RWNESITALLIGLCTGVVILLMTKGS 73

Db 55 TEEMSSAULEMULLLSALNSYYTOKRRAVHEVTLISFYGMIGLITRMSPHYI 114

Qy 74 SHLFVSESDLFFTYLPLPPIENAGFOVKKOFRNFNTITLGAVGTMISFFTISTAAIA 133

Db 115 QDTVTFFSYYFFNVNLLPPIILNGYENQVNENNMISLIFAIPEGFISAVVGI-ILY 173

Qy 134 IFSRMNIGTLDV - -GDEFLAIGALESATSDVCFLQVLQDET - -FLYSLVEGVVNDAT 190

Db 174 IWFILGLESIDISFADMSVGTLSATDPVTLSISFYAKYVDPLKTYTGFSSLNDAIS 233

Qy 191 IVLFLNALQNFDLVHIDAVVLKFLGNFYLFLSSTSFLGVFAGLSSVTLKLYTGRHSTD 250

Db 234 TWMFETOCFKHGPATPSVFEGAGLFLMTFSVSLJGVLIGLVALIKTHIRR - -PQ 292

Qy 251 REVALMLMAYLSYMLNLLDLSGILVTFECGVLMHSYTHWNTESSRVTKHAFATLSE 310

Db 293 IESCLLILIAYESYFFNGCHMSGIVSLLFCGTLKHYAYNMSRSQSQITKYTFQLLAR 352

Qy 311 TAETFLFLYGMMDAL-DIEKWEFAASDRPGKSIGISSLILGL---VLIJGRAEVFPLS-- 363

Db 353 LSENFTIYLGLELFTEVE-----LYVKPLIIVLAAISCVARNCAVFPQSQF 400

Qy 364 -----FLSNLTTK --APNEKITWROQVVIWAGLMRGAYSIALAYN---KF 404

Db 401 VNIWIYRKVTTISMSGIUGENTSVPDPE IPYNNQMMTFWAGL-RGAYGVALALGIOQEYKF 458

Qy 405 TRSGHTQLHGNAIMTSTITYVLFSTMVGMMTKPLLRLPLPASGHPVTSEPSPK - -SL 462

Db 459 T-----LIATVLYVVVLTIVI FGGTAGMLEVNIKTG-CISEDDTSDEDFD 505

Qy 463 HSP-LLTSMQGSDLE-----STT----- 479

Db 506 EAPRATNLNSQHNTQDLPGSDNNNSPDISDQFAYSNKNLUPNNTSTGGNTFGGLNET 565

Qy 480 -----NIVRPS---SLRMLLTQPTVHYYWRKFDDALMRPMF 514

Db 566 ENTSPNPARSSMDKRNLDKGTTNSDQWQNDFDQVLPVF 609

RESULT 11
US-10-217-096-6
; Sequence 6, Application US/10217096
; Publication No. US2003004933A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J., Ferriera, Holly M.
; TITLE OF INVENTION: 96895, A Human Sodium Hydrogen Exchanger
; TITLE OF INVENTION: Family Member and Uses Therefor
; FILE REFERENCE: MP10-147P1RM
; CURRENT APPLICATION NUMBER: US/10/217,096
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 60/312,544
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 6
; LENGTH: 896
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Homo sapiens
US-10-217-096-6
; Query Match 17.8%; Score 485; DB 9; Length 896;
; Best Local Similarity 29.9%; pred. No. 3e-34;
; Matches 155; Conservative 93; Mismatches 190; Indels 80; Gaps 22;

Qy 22 VVSINLFVALLCACIVLGHLLEE - -RWNESITALLIGLCTGVVILLMTKGS 80

Db	49 LVALWILVIASTIAK--IVPHLSRKVTSVLVPECLLILLGIVLGIVLGGIVLAVAKKAAYQL---E 103	Db	215 VCLVGEGQINNIGLLDTLLFGSIISAVDPVAVVAVFBEIHINELLHLVFGESLUNDAVT 274		
Qy	811 EDLFFFLYLPLPPIFLINAGFQVKKKQFFERNFMITLFGAVCTMISFTISSA-----AIAT 134	Qy	191 IVLENALO--NEDLVHWDAAVVLKPLQSNFFPLFLFSSSTFLGFAGLSSAYIKKLIGRH 247		
Db	104 PGTFFLFLPLPPIVLDSGYPPSRLEFDNDGAILTYAVVETLWNAAFTTGALMGLOQAGIV 163	Db	275 VVLYHLPFFEFANDSISGI--SDIFLGLFL-SFFVVAFLGGVFGVYGVIAFTSR--FTSH 329		
Qy	135 FSRMRNIGTLVDGFELAIGAFSAIDSVCVTLQVLNQ--DETPFLPSLYFEGCVVNDATSI 191	Qy	248 STDREVALMMLMAYLSYMAELLDLSGILTVFECIGIYMSHTYWHNTPESSRVTTKHFAT 307		
Qy	152 APRVQAGL--DDEFLGFLSISAVDPVAVLAVFEEHVNET--LFIIVGESLINDAVT 218	Db	330 IRVFLPEFLFLYSMAYLSAELFLHSGSMALLASGVMWPRPYEANIKSHMTTIKFELKM 389		
Db	164 VLFNALQNF--DLVHDAAVVFLKPLGNFPLFLSSTLG-VFEGL--ISAYTIKKLYIG 245	Qy	308 LSFAITELFLFLYGMDAL-DIEKWFASDRPGKSIGISSIILGLVILIGRAAFVFLPSFLS 366		
Qy	192 VLFNALQNF--DLVHDAAVVFLKPLGNFPLFLSSTLG-VFEGL--ISAYTIKKLYIG 245	Db	390 WSSSETLFLFIFGVSYTAGSHOWNW----TIVISTLL--FCCLARVQLVLTWFI 440		
Db	219 VLYKVCNSFVEMGSANVQADYDLYKGVASLFLVSGGAAGVGLYFAFLAATTRFTKVRKI- 277	Qy	367 NLTKAPNEKITWQOQVIVWAGLARGAVSIALAYNKFRSGHTQHGNIAIMITSTVVY 426		
Qy	246 RHSTDREVALMMLMAYLSYMAELLDLSGILTVFECIGIYMSHTYWHNTPESSRVTTKHF 305	Db	441 N--KERTVKLTPKDQFTIAYGGL--RGATAFSIGY--LMDKXHEPMD--LFLTAIIIVI 492		
Db	278 --LEPLVFLLAYAAVLAEMASLTLAVTMCGCKKYEANISHKSRTVKT 332	Qy	427 LFSTMVFGMMTKPLIRLPLLPSGHPTSESSPKSLHSPLTSMOGSDELSTTNIVRPPS 486		
Qy	306 ATLSFETAETFLFLYGMDAL-DIEKWFASDRPGKSIGISSIILGLVILIGRAAFVFL 362	Db	493 EFTVYQGNTTIRPLDLL----AVKVKQETRSINBEIHTQFLDHILTGEDIC--- 542		
Qy	336 KTLASCAETVFMFLGJISAVDSSKAWD-----SGLVGLTLLFLFRLGVVLIQ 382	Qy	487 LRMLTKPHTPVVYWKEDDALMR 511		
Db	333 TWLNQFLRVLPLDKI--DQVMSYGL--RGAVAFALV---ILLDRTRVPKAQDFYAVTT 434	Db	543 -----GHYGHHHWK--DKLNR 556		
Qy	423 ITVVLFSTMVEGMMTKPLIR-LLLPASGHPTSESSPKSLHSPLTSMOGSDELSTNNI 481	RESULT 13			
Db	435 IIVVFFTVTVOGLTIRKPLVWKLVKVRKSE--HKTTLNQEULHEHTEDH1---LAAVEDV 487	US-09-800-729-215			
Qy	482 VRPSSLRMLLTKTPHTVHYY--WRFKD---DALMR 511	Sequence 215, Application US/09800729			
Db	488 V-----GHGHGHYIWRDRWEQFDKKYLSQLLMR 514	; Patent No. US20020068319A1			
RESULT 12					
; Sequence 3, Application US/09824734					
; Patent No. US200200683485A1					
; GENERAL INFORMATION:					
; APPLICANT: ZHU, JIAN-KANG					
; APPLICANT: SHI, HUAZHONG					
; APPLICANT: ISHITANI, MANABU					
; APPLICANT: STEVENSON, BECKY					
; TITLE OF INVENTION: PROTEINS AND DNA RELATED TO SALT TOLERANCE IN PLANTS					
; FILE REFERENCE: 2056440520					
; CURRENT APPLICATION NUMBER: US/09/824734					
; CURRENT FILING DATE: 2001-04-04					
; PRIOR FILING DATE: 2000-04-04					
; SEQ ID NO 3					
; LENGTH: 822					
; TYPE: PRT					
; ORGANISM: Cricetulus griseus					
; US-09-824-734-3					
Query Match Score 11.58; DB 10; Length 370;					
; Sequence 3, Application US/09824734					
; Patent No. US200200683485A1					
; CURRENT APPLICATION NUMBER: US/09/824734					
; CURRENT FILING DATE: 2001-04-04					
; PRIOR FILING DATE: 2000-04-04					
; NUMBER OF SEQ ID NOS: 20					
; SOFTWARE: Patentin version 3.1					
; SEQ ID NO 3					
; LENGTH: 822					
; TYPE: PRT					
; ORGANISM: Homo sapiens					
; US-09-824-734-3					
Query Match Score 11.58; DB 10; Length 822;					
; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
Query Match Score 17.6%; DB 10; Length 822;					
; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
Query Match Score 11.58; DB 10; Length 822;					
; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
Query Match Score 11.58; DB 10; Length 822;					
; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
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; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
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; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
Query Match Score 11.58; DB 10; Length 822;					
; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
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; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
Query Match Score 11.58; DB 10; Length 822;					
; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
Query Match Score 11.58; DB 10; Length 822;					
; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
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; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
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; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
Query Match Score 11.58; DB 10; Length 822;					
; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
Query Match Score 11.58; DB 10; Length 822;					
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; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
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; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
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Query Match Score 11.58; DB 10; Length 822;					
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; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
Query Match Score 11.58; DB 10; Length 822;					
; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
Query Match Score 11.58; DB 10; Length 822;					
; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
Query Match Score 11.58; DB 10; Length 822;					
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; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
Query Match Score 11.58; DB 10; Length 822;					
; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
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; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
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; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
Query Match Score 11.58; DB 10; Length 822;					
; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
Query Match Score 11.58; DB 10; Length 822;					
; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
Query Match Score 11.58; DB 10; Length 822;					
; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
Query Match Score 11.58; DB 10; Length 822;					
; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;					
Query Match Score 11.58; DB 10; Length 822;					
; Best Local Similarity 28.7%; Pred. No. 1..le-33; Mismatches 101; Indels 58; Gaps 19;					
; Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 1					

Qy	403	KFTRSGHTOLHGNAIMITSTIVVLFSTNV	432	R; Harris, B. submitted to the EMBL Data Library, December 1998
Db	421	KFTFRAGHTDVRGNAMITSTIVCLFLSTVV	450	A; Reference number: Z22848 A; Accession: T22848 C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
RESULT 2				
	T22848	hypothetical protein F57C7.2 - Caenorhabditis elegans		
	C; Species: Caenorhabditis elegans			
	C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000			
	A; Status: preliminary; translated from GB/EMBL/DBBJ			
	A; Accession: T22848			
	A; Reference number: Z19625			
	A; Molecule type: DNA			
	A; Cross-references: EMBL:Z69646; PIDN:CAA93476..1; GSDB:GN00028; CESP:F57C7.2			
	A; Experimental source: clone F57C7			
	C; GenBank ID: Y18D10A.6			
	A; Gene: CESP:Y18D10A.6			
	A; Introns: 23/3; 56/1; 103/2; 246/3; 352/3; 492/2; 578/3			
	Query Match Score 20.78;	Score 564.5;	DB 2;	Length 703;
	Best Local Similarity 34.28;	Pred. No. 6.8e-34;		
	Matches 156;	Conservative 83;	Mismatches 168;	Indels 49;
	Gaps 16;			
Qy	7	AARLGALYTSDASVVSINLFVALCACIVLGHLEENWNESENITALLIGCTGVVIL	66	
Db	118	AAIVGNVSEBEKRSLAIFPTLVMLATLVHMLIVSKHMPESLAVVALGALG-STL	176	
Qy	67	LMTKGKSSHLFLVPSEDLEFFYLPLPPIINAGFOVKKKOFFRNFMNTILEGAVGTMISFPT	126	
Db	177	SYRRDWEEIALESPDFVLFLVLPPLPENAYNLNKGYFFSNFVPLTFAIFGTTISAMV	236	
Qy	127	ISAAIAIAIFSRMNRNIGTDVGDF---LAIGAATFSVCLQLVNODET-PFLYSLVF	180	
Db	237	IG AGLVILGAIGL---IFETEFFECFAAMISADPVGTLAIFPAKVSESSLVLMVLF	291	
Qy	181	ENALQNFDLVIHTDAAVVVLKFLGNNFFYFLSSTFLGV	229	
Db	292	GESMLNIAVASIVLAAATLRHAKPSFNLSLPAE1-ITSAFV---TETEMEFFSACLVG	344	
Qy	230	FGAILSLAYTKLGYIGHSTDEVALNMFLSYMAELDSLGLITVEFGIVMSHYT	289	
Db	345	GIGLGSALLFKHVDL-RKTPSLEFLALIIFSTIYGGAELDLSGMALFGISMQFT	403	
Qy	290	WHNTTESSRVTKHAFAFLTSFTAETFLFLYVGMDALLEKWEFAASDRPGKSTGISSLLG	349	
Db	404	RHNVSPQAQTFRHTFTISVAETSFAYGMAFFI-T-KLNFA---PWLJFWSVV-	545	
Qy	350	LVLIGRAFYFPLSFLSNTLKKAPNEKITWROQVVIWAGLMRGAYSIALA-YNKFTRSG	408	
Db	456	LCLGRACANVPLAYLNQCRK-DVQISMKNQIWFMSG-MRGAVCFALVYMDLDK--	510	
Qy	409	HTQLHGNAMITSTIVVFLVTFMTPKJIRLL 444		
Db	511	--EKSKILLTTVFLILFIFTFLGGSAFLFISFI	542	
RESULT 4				
	T37706	probable sodium/hydrogen exchanger - fission yeast (Schizosaccharomyces pombe)		
	C; Species: Schizosaccharomyces pombe			
	C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000			
	R; Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.			
	A; Reference number: T37706			
	A; Accession: T37706			
	A; Status: preliminary; translated from GB/EMBL/DBBJ			
	A; Molecule type: DNA			
	A; Residues: 1-569 <MUR>			
	A; Cross-references: EMBL:Z97208; PIDN:CA010103..1; GSPDB:GN00066; SPDB:SPAC15A10..06			
	A; Gene: SPAC15A10..06			
	A; Map position: 1			
	A; Introns: 11/1; 116/3; 356/3			
	C; Superfamily: hypothetical protein yvgp			
	Query Match Score 20.3%;	Score 552;	DB 2;	Length 569;
	Best Local Similarity 29.4%;	Pred. No. 4.4e-33;		

Matches 148; Conservative 113; Mismatches 195; Indels 48; Gaps 15;	Db 174 IWFFIGLESIDISPADAMSVGATLSATDPVITLISIFNAVKVDPKLYTILFGESIILNDALIS 233
Qy 27 LEVALLOCACIVIGHLL-----EENRWNNSITALLIGCTGVWILLMKGSSHLPVF 79	Qy 191 IVFLNALQNDLVHIDAUVYKELGFNFEEYLFLSSTELGYFAGLISAYIKKLYIGRHSTD 250
Db 37 LFILV-----LLIGALITSYYSQSKKTRAIHETVSVFGMVGLLIRSPGLITIONMVSF 93	Db 234 IVMFETCOKFHGPATFSSYFEGACLFMTFSVSLIGLIGLVLALLKHTHRY-PQ 292
Qy 80 SEDLFFTYLLPPLIFNGFQYKKQPFERNFMTITLEGAUTGMISFTTIAAIAIFSRMN 139	Qy 251 REVALMLMAYLMSYMAELLDLSGLTIVFECGIVWISHYTHWNNTESRYTTKHFATLSD 310
Db 94 HSTEFFNVLPLPILNGSEYEHQSNSFRNIGLTFAFPTFISNYTLGV-LVYIFSFN 152	Db 293 FESCLLILAYEPEFSNGCHMSGVSLFCGTTKHAYAYNNRSQSTIKYIEQLQ 352
Qy 140 IGTLDVG--DFAIAGTAISDVTCLQVLNQ---DETPFLSIVFEGYVNDATSVLFL 194	Qy 311 IAETFLFLYVGMDAL-DIEKWEFAASDRPGKRSIGISITSLIGL---VLGRAAFVPELIS- 363
Db 153 FENLSMTEVAISMGATLISADPVTVAIAFNSYKVQK--LYTIFGESIUNDAIVMF 210	Db 353 LSENFFIFIYGLGLELVE-----LVKPPLTVAAISICARWCAYFPLSQF 400
Qy 195 NALQNEDVHIDAUVYKELGFNFEEYLFLSSTELGVNGFAGLISAYIKKLYIGRHSTDREVA 254	Qy 364 -----ELSMUTKK---APNEKJITWROQVVYIWAGLMRGAVSIALAYN----KF 404
Db 211 ETLQQFOGKTGHFTFLSGSIGFIFTFFISLIGVSIGLTALLKLYSRRYPS-TESC 269	Db 401 VNWIYTRVKTIRSMMSGTGENTSVPDE-IPVNQMTFWAGL-ROAVGVALALGQGEYKF 458
Qy 255 LMLMLMAYLMSYMAELLDLSGLTIVFECGIVWISHYTHWNNTESRYTTKHFATLSEIAT 314	Qy 405 TRSGHTQLHGNIAIMTSTIVTIVLFLSTMFCGMMTKPLIRLULLPAAGHPVTEPSSPK-SL 462
Db 270 FIFTYLSFTYFSNGCIMGSVVSLLFCGTTKHAYAFNSYKAKLSTKYFRLAQSEN 329	Db 459 T-----UATVLYVWVLTIFGTTAGMLEVNUKTC-CISEEDTSDEFPI 505
Qy 315 FLFLYVGMDAL-DIEKWEFAASDRPGKRSIGISISSLGLVLAIRGAFA--VFPFLSLSNTKFA 372	Qy 463 HSP-LLTSMGDSLE-----STR----- 479
Db 330 FIFTYLSFTYFSNGCIMGSVVSLLFCGTTKHAYAFNSYKAKLSTKYFRLAQSEN 329	Db 506 EAAPRANLNLSSSITOTDGPYSDNNNSPDISIDQFAVSSNKLPNNNISTGGNTFGGLNET 565
Qy 373 PN---EKITWROQVVYIWAGLMRGAVSIALAYNKTFRSGHTQLHGNIAIMTSTIVLFL 428	Qy 480 ----NIVRPS---SLRMLLTKPTHTVHYWKRKDALLMRPMF 514
Db 381 RGNLNLIDIPYSQMMLFWAGL-RGAVGVALAAGFEGENAOY-----LRTATLIVVVVL 432	Db 566 ENTSPNPARNPARSSMDKKRNLRDKGT1FNNSDOWFQNDEQVLKPVF 609
Qy 429 STMVFGMMTKPLTRLLEASHGPVTEPSSPKSLHSPLTSMQGSDLESTINTVRESSLR 488	RESULT 6
Db 433 TLIFGGSTARMLTLEASHGPVTEPSSPKSLHSPLTSMQGSDLESTINTVRESSLR 490	A40205 Na+/H+ -exchanging protein 3 - rabbit
Qy 489 MLITKPTHTVHYWKRKDALLMRP 512	N; Alternative names: Na+/H+ antiporter
C; Species: <i>Saccharomyces cerevisiae</i>	C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002	C; Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 05-Nov-1999
C; Accession: S69734	C; Accession: A40205
R; Dietrich, F S	R; Brant, S.R.; Walker, M.S.; Pouyssegur, J.; Donowitz, M.
A; Reference number: S69734	A; Reference number: A40205
A; Molecule type: mRNA	A; Accession: A40205
C; Superfamily: hypothetical protein yggP	A; Cross-references: GB:MB87007; NID: 9165548; PMID:AAA31420.1; PID:9165549
Submitted to the EMBL Data Library, August 1995	C; Cross-references: GB:MB87007; NID: 9165548; PMID:AAA31420.1; PID:9165549
A; Description: The sequence of <i>S. cerevisiae</i> lambda 3641 and cosmids 9461, 9831, and 941	C; Keywords: transmembrane protein
A; Reference number: S69735	Query Match Score 18.1%; Best Local Similarity 31.38%; Pred. No. 1.8e-28;
A; Map position: 4R	Matches 143; Conservative 91; Mismatches 171; Indels 52; Gaps 18;
C; Superfamily: hypothetical protein yggP	Query Match Score 18.1%; Best Local Similarity 31.38%; Pred. No. 1.8e-28;
A; Residues: 1-633 <DIE>	Db 57 IALWLVLVASLAKTIVFHLSHKVTSVYVPESSALLIVLGLVLLGGIVL-----AADHIASTFTLTP 111
A; Cross-references: EMBL:U33007; NID:9927685; GSPDB:GN00004; MIPS:YDR456w	Qy 25 INLFVALLCACVGHLLEE-NRWVNESITALLIGCTGVVLLMTKGKSSHL-FVVFSE 81
C; Genetics:	Db 57 IALWLVLVASLAKTIVFHLSHKVTSVYVPESSALLIVLGLVLLGGIVL-----AADHIASTFTLTP 111
A; Gene: SGD:NHX1; MIPS:YDR456w	Qy 82 DLFITVLLPPLTFNAGQVKRQFERNEMTFLFGAVGTMQFSTISIAAIAIFSMNQ 141
A; Cross-references: SGD:S0002864	Db 112 TVFFFYLLPPLTFNAGQVKRQFERNEMTFLFGAVGTMQFSTISIAAIAIFSMNQ 141
C; Superfamily: hypothetical protein yggP	Db 172 EULKGLIDFLFGSLLIAVDPAVLAFFEEHVNEVFLTIVGESELINDAVTVVNVQF 231
Qy 16 TSDYASVSYINLYVALLCACIVGHLLDEN-FRWVNESTITALIIGLCTGVVLLMPKGKS 73	Qy 199 NFDLVHIDAAV--VLFKLGNFFYFLSLSSTFLG-VFAGLISAYIKKLYIGRHSTDREVA 254
Db 55 TEEMFSSWAIFMULLLTSALWSSYLLQKRRAVHETVLSIFYGMVIGLIRMSPHYI 114	Db 232 SFVTLGGDKRVTGCVKGIYSEFVSVLGGTLYGVWVAFLLS-LVTR--FTKHYVIEPG 287
Qy 74 SHLFVFSDELFFYLLPPLIFNAGEQVKKKOFFERNEMTFLFGAVGTMISFPTISTAAIA 133	Qy 255 LMMLMAYLMSYMAELLDLSGLTIVFECGIVWISHYTHWNNTESRYTTKHFATLSDIAET 314
Db 115 QDTVTFNNSYFFENVLLPPTILNSCYELQVNFTNNMLSLIFIAPIGFISAVVIGI-ILY 173	Db 288 FVFIISLVSILTSEMLSSILATFEGCICOKYKANISEQSATIVRYTMKMLSAET 347
Qy 134 IFSRNNIGTLDV--GDFFLAIGATISATSVCTLOVLNGDET-PFLYSLVFGEGVWNDATS 190	

Qy	365	LSNLTKKAPNEKITWROQVYVWAGLMRGAWSIALAYNKFTRSGHTQLHGNAIMITSIT 424	RESULT 10
Db	435	FIN-- KFIRVKLTPDQFLIAYGL - RGAIAFSGLY - LLDKKKHPM6D - IELTATIT 486	A46748 Na+/H ⁺ -exchanging protein NHE-2 ; rat
Qy	425	VVLFSTMFGMMTKPLIRLILPASGHPTNSEPSSPKSLHSPLTSMQSDLESTTNIVR 484	C; Species: Rattus norvegicus (Norway rat)
Db	487	VIFFTVFGQMTIPRLVLDL-----AVKKOETKRSTINEEHTQFDLHLTGIEDIC- 538	C; Date: 03-May-1994 #text_change 03-May-1994 #text_change 05-Nov-1999 C; Accession: A47449 R; Wang, Z.; Orlowski, J.; Shull, G.E. J. Biol. Chem. 268, 11925-11928, 1993 A; Title: Primary structure and functional expression of a novel gastrointestinal isoform of a Na ⁺ /H ⁺ -exchanging protein 3 - rat A; Reference number: A46748; MUID:93280160; PMID:7685026
Qy	485	SSLRMILTKPHTVHYWYKPFDDALMR 511	A; Status: preliminary
Db	539	----- GHYGHWWK -- DKLNR 552	A; Molecule type: mRNA A; Residues: 1-813 <WAN> A; Cross-references: GB:L11216; PID:9205318; PMID:AAA72350_1; PID:9205319 R; Collins, J.P.; Honda, T.; Knobel, S.; Bulus, N.M.; Conary, J.; DuBois, R.; Ghishan, F.; Proc. Natl. Acad. Sci. U.S.A. 90, 3938-3942, 1993 A; Title: Molecular cloning, sequencing, tissue distribution, and functional expression of a Na ⁺ /H ⁺ -exchanging protein 3 - rat A; Accession: A47449 A; Reference number: A46748; MUID:93240205; PMID:7683411
Qy	B40204	Na ⁺ /H ⁺ -exchanging protein 3 - rat	A; Status: preliminary
Db	540	Alternative names: Na ⁺ /H ⁺ antiporter	A; Molecule type: nucleic acid A; Residues: 117-813 <COL>
Qy	424	N;Species: Rattus norvegicus (Norway rat)	A; Experimental source: intestine
Db	541	C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 05-Nov-1999	A; Note: sequence inconsistent with the nucleotide translation from NCBI backbone (NCBIN:130778, NCBIPI:130779)
Qy	425	R;Orlowski, J.; Kandasamy, R.A.; Shull, G.E.	A; Status: preliminary
Db	542	J. Biol. Chem. 267, 9331-9339, 1992	A; Molecule type: nucleic acid A; Residues: 117-813 <COL>
Qy	426	A;Title: Molecular cloning of putative members of the Na/H exchanger gene family. cDNA c	A; Experimental source: intestine
Db	543	A;Related proteins: A40204; MUID:92250539; PMID:1577762	A; Note: sequence extracted from NCBI backbone (NCBIN:130778, NCBIPI:130779)
Qy	427	A;Status: preliminary	Query Match 17.6%; Score 479; DB 2; Length 813;
Db	544	A;Molecule type: mRNA	Best Local Similarity 27.3%; Pred. No. 1.6e-27;
Qy	428	A;Cross-references: 1-831 <ORL>	Matches 141; Conservative 95; Mismatches 206; Indels 80; Gaps 19;
Db	545	A;Keywords: transmembrane protein	Query 16 TSDYASV --VSINFEVLLACTVGLHLLNE-RWNNNESITALIGLCTGVVILLMTK 71
Qy	429	Query Match 17.7%; Score 480.5; DB 2; Length 831;	Query Match 17.6%; Score 479; DB 2; Length 813;
Db	546	Best Local Similarity 28.6%; Pred. No. 1.3e-27;	Best Local Similarity 27.3%; Pred. No. 1.6e-27;
Qy	430	Matches 146; Conservative 101; Mismatches 197; Indels 67; Gaps 19;	Matches 141; Conservative 95; Mismatches 206; Indels 80; Gaps 19;
Db	547	Qy 22 VVSINFEVLLACIV-LGHLEENRNWNESITALLIGLCTGVVILLMKGKSSH- TV 78	Query 17 TSDYASV --VSINFEVLLACTVGLHLLNE-RWNNNESITALIGLCTGVVILLMTK 71
Qy	431	DB 54 IIAIWILVASLAKIVPHSH - KVTSVYPEEALIIVGIVLGGI----WAADHIAST 106	Query 17 TSDYASV --VSINFEVLLACTVGLHLLNE-RWNNNESITALIGLCTGVVILLMTK 71
Qy	432	Qy 79 FSEBLDEFTYLLPPTIFNPAFQVKKOFFRFNMITLFGAVGTMISFTISTAA 138	Query 17 TSDYASV --VSINFEVLLACTVGLHLLNE-RWNNNESITALIGLCTGVVILLMTK 71
Db	548	DB 107 LTPTLFFYLLPPTIVDAGYMPNRLFFGNLTGILLYAVIGTIWAAATGCLSLYGVFLSG 166	Query 17 TSDYASV --VSINFEVLLACTVGLHLLNE-RWNNNESITALIGLCTGVVILLMTK 71
Qy	433	Qy 139 NIGLDVG --DFAAIGAFSATSVDYCTQVLNQ - DTFPLFLYSLVFGEGYVNDATSVLFN 195	Query 17 TSDYASV --VSINFEVLLACTVGLHLLNE-RWNNNESITALIGLCTGVVILLMTK 71
Db	549	DB 167 LMGELKIGLDDFLPGLSIIAAYDPVAVLAEVEHVNEFLIVGESELINDAVLVLN 226	Query 17 TSDYASV --VSINFEVLLACTVGLHLLNE-RWNNNESITALIGLCTGVVILLMTK 71
Qy	434	Qy 196 ALONFDLVIHDARAV --VLFKLGNYFLYFLPSLSTFLGV - FAGLSSAYIYKLYIGRHSTD 251	Query 17 TSDYASV --VSINFEVLLACTVGLHLLNE-RWNNNESITALIGLCTGVVILLMTK 71
Db	550	DB 227 VPSFSTVIGDAVTGCVKGIVSFVSLGTLVCFIAFLLS - LTVR - FPKHVR 282	Query 17 TSDYASV --VSINFEVLLACTVGLHLLNE-RWNNNESITALIGLCTGVVILLMTK 71
Qy	435	Qy 252 EVAIIMMLMAYLSYMLAELDLISGLTIVFECGLVMSHTWNVTESSRVTKHFATLTSFI 311	Query 17 TSDYASV --VSINFEVLLACTVGLHLLNE-RWNNNESITALIGLCTGVVILLMTK 71
Db	551	DB 283 EPGFVFVSYLSYLTSEMMLSAILAITFCGCCCKYVKANISEQSATVRYTMKMLASG 342	Query 17 TSDYASV --VSINFEVLLACTVGLHLLNE-RWNNNESITALIGLCTGVVILLMTK 71
Qy	436	Qy 312 AETFLFLYVGMDALIEWEFASDRGKSIGISSILGLVILG - -RAAFVFPFLSLSNLT 369	Query 17 TSDYASV --VSINFEVLLACTVGLHLLNE-RWNNNESITALIGLCTGVVILLMTK 71
Db	552	DB 343 AETLFLFLYVGMDALIEWEFASDRGKSIGISSILGLVILG - -RAAFVFPFLSLSNLT 369	Query 17 TSDYASV --VSINFEVLLACTVGLHLLNE-RWNNNESITALIGLCTGVVILLMTK 71
Qy	437	Qy 370 KKAPNEKITWROQVYVWAGLMRGAWSIALAYNKFTRSGHTQLHGNAIMITSITVVLFS 429	Query 17 TSDYASV --VSINFEVLLACTVGLHLLNE-RWNNNESITALIGLCTGVVILLMTK 71
Db	553	DB 394 RMYQLETI ---DQVMSYGGL - RGAYAYALV ---VLDDEKKVKEKNFLVFSVTLIVVFT 445	Query 17 TSDYASV --VSINFEVLLACTVGLHLLNE-RWNNNESITALIGLCTGVVILLMTK 71
Qy	438	Qy 446 VLFQGLTIPLYQWLKVSRSE - QREPKLNELKGRADFHTLSATEDISGQIGHNYLRDK 503	Query 17 TSDYASV --VSINFEVLLACTVGLHLLNE-RWNNNESITALIGLCTGVVILLMTK 71
Db	554	Qy 486 SLRMLLTKPHTVHYWYRKFD ---DALMR 511	Query 17 TSDYASV --VSINFEVLLACTVGLHLLNE-RWNNNESITALIGLCTGVVILLMTK 71
Qy	505	Db 504 ----- WSNFDRKFLSKVLMR 518	Query 17 TSDYASV --VSINFEVLLACTVGLHLLNE-RWNNNESITALIGLCTGVVILLMTK 71

RESULT 11

S30198

Na⁺/H⁺-exchanging protein - Chinese hamsterN;Alternate names: Na⁺/H⁺ antiporter; Na⁺/H⁺ exchanger

C;species: Cricetulus griseus (Chinese hamster)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
 C;Accession: S30198; S29341
 R;Counillon, L.; Pouysseur, J.
 B;Title: Nucleotide sequence of the Chinese hamster Na(+) / H(+) exchanger NHE1.
 A;Reference number: S30198; MUID:93192332; PMID:8383540
 A;Accession: S30198
 A;Molecule type: mRNA
 A;Residues: 1-682 <cDNA
 A;Cross-references: GB:MB96331; NID:9164595; PIDN:AAA310921; PID:9164596
 C;Genetics:
 A;Gene: NHE1
 C;Keywords: glycoprotein; ion transport; membrane protein
 F;76.374,414/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.6% Score 478; DB 2; Length 822;
 Best Local Similarity 28.7%; Pred. No. 2e-27;
 Matches 145; Conservative 101; Mismatches 201; Indels 58; Gaps 19;

QY 18 DYASV--VSINLFWVALCACIVLGHLEE-NRKYNESTALIIGLCTGVVILLMTGKS 73
 DB 99 DYLIVRTTPFFISLWLLACIMKIGFHVIITISSIVPESCLIVVGLYGLI---KVG 154
 QY 74 SHLFVFSEDLFIFYLPLPIFNAGFQVKKKQFFRNFMITLFGAVGTMISFTLIS--IAA 131
 DB 155 ETPPFQLSQDVFPLFLPPITLDAGYFLPLRQTENLGTLLFAVGTGLWNAAFFGGLYA 214
 QY 132 IAFSRMNIGTLDVDFLTAIGFATSDVCTLGVLQDNDE-TPLFLSYVEGVVNNDATS 190
 DB 215 VCLVGGEQINNIGLDTLLFGSISLAVDPEVAVAVFEETHINELLHLVGEISLNDAVT 274
 QY 191 IVLFNALQ--NFDLVHIDAAYVVLKFLGNFNFYLFLSSTFLGVFAGLSSAYIKKLYIGRH 247
 DB 275 VVLYLHFEENFDIGI SDIFGFL SFPVVALGGVFGVYGVIAFTSR--FTSH 329
 QY 248 STDREVALMLMAYLSYMIAELDSGLTIVFFGIVMSHTWHNTTESSRYTTKHAFAT 307
 DB 330 IRVTEPLFVFLYTSMAYLSAELPHLSGMALIASGVVAPRYANISHSHTTIKYFLRM 389
 QY 308 LSFTAETEFLYNGMDAL-DIEKWEFASDRPGKSIGISSLGLVIGRAAFVPLSL 366
 DB 390 WSSSETLFLIFLGVSTAGSHQNW----TFVISTL--FCLLARVIGLVLTWF 440
 QY 367 NLTKAPNEKITWRQQVIIWAGLRLGAVSIALAYNKTRSGTOLHNAIMTSTTV 426
 DB 441 N---KERIVKLTKPKDQFIAYGSL-RGATPSY--LMDKRPFKPMCD--LIFTAIVI 492
 QY 427 LFSTMVFGMTKPLIIRLPLPASHGPVTSEPPSPKSLHSPLSMQGSDELSTTN 486
 DB 493 FTTVFGQGMTRPLVDL--AVKKKQETRSINEEHTQFLDHLLTGIEDC---- 542
 QY 487 LRMLLTKEPTHTHYWYRKFDALMR 511
 DB 543 -----GHYHHHWK---DKLNR 556

RESULT 13
 157487 Na+ / H+ - exchanging protein, amiloride-sensitive - human
 N;Alternative names: Na+/H+ antiporter; NHE-1
 C;Species: Homo sapiens (man)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Oct-1999
 R;Pieleg, L.; Dyck, J.R.; Wang, H.; Fong, C.; Haworth, R.S.
 Mol. Cell. Biochem. 125, 137-143, 1993
 A;Title: Cloning and analysis of the human myocardial Na+/H+ exchanger.
 A;Reference number: 157487; MUID:94111706; PMID:8283968
 A;Accession: 157487
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-815 <FLI>
 A;Cross-references: GB:S68616; NID:9544775; PIDN: AAC606061; PID:9544776
 R;Zardes, C.; Franchi, A.; Pouysseur, J.
 Cell 56, 271-280, 1989
 A;Title: Molecular cloning, primary structure, and expression of the human growth fac
 A;Reference number: A31311; MUID:89106219; PMID:2536298
 A;Accession: A31311
 A;Molecule type: mRNA

R;Reilly, R.F.
 Am. J. Physiol. 261, 1088-1094, 1991
 A;Title: cDNA cloning and immunolocalization of a Na+ / H+ exchanger in LLC-PK1 renal e
 A;Reference number: 146613
 A;Accession: 146613
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-682, H⁺, 684-818 <RE2>
 A;Cross-references: GB:MB96331; NID:9164595; PIDN:AAA310921; PID:9164596

Query Match 17.5% Score 476; DB 2; Length 818;
 Best Local Similarity 29.2%; Pred. No. 2.7e-27;
 Matches 149; Conservative 99; Mismatches 193; Indels 70; Gaps 20;
 QY 18 DYASV--VSINLFWVALCACIVLGHLEE-NRKYNESTALIIGLCTGVVILLMTGKS 73
 DB 95 DYTHRTPPFESLWLLACIMKIGFHVIITISSIVPESCLIVVGLGLIKAVGE-- 151
 QY 74 SHLFVFSEDLFIFYLPLPIFNAGFQVKKKQFFRNFMITLFGAVGTMISFTLIS--IAA 131
 DB 152 TPPFLQSE-VFELFLPFLPILDAFYPLPQQTENLGTLLFAVGTGLWNAAFFGGLMYA 210
 QY 132 IAFSRMNIGTLDVDFLTAIGFATSDVCTLGVLQDNDE-TPLFLSYVEGVVNNDATS 190
 DB 211 VCLVGGEQINNIGLDTLLFGSISLAVDPEVAVAVFEETHINELLHLVGEISLNDAVT 270
 QY 191 IVLFNALQ--NFDLVHIDAAYVVLKFLGNFNFYLFLSSTFLGVFAGLSSAYIKKLYIGRH 247
 DB 271 VVLYLHFEENFDIGI DVFVGLF SFPVVALGGVFGVYGVIAFTSR--FTSH 325
 QY 248 STDREVALMLMAYLSYMIAELDSGLTIVFFGIVMSHTWHNTTESSRYTTKHAFAT 307
 DB 326 IRVTEPLFVFLYTSMAYLSAELPHLSGMALIASGVVAPRYANISHSHTTIKYFLRM 385
 QY 308 LSFTAETEFLYNGMDAL-DIEKWEFASDRPGKSIGISSLGLVIGRAAFVPLSLF 364
 DB 386 WSSSETLFLIFLGVSTAGSHWNTWFV-----ISTL--FCLLARVIGVLGTW 434
 QY 365 LSNLTKKANEKWTWRQQVIIWAGLRLGAVSIALAYNKTRSGTOLHNAIMT 420
 DB 435 FIN--KFRIVKLTPKDQFTIAVGGL-RGAIAFSLGHLDKNHFPMC-----LFT 482
 QY 421 STTVVLFLSTIVFGMMTKPLIIRLPLPASHGPVTSEPPSPKSLHSPLSMQGSDELSTTN 480
 DB 483 ALITVVFIVFVQGMTRPLVDL--AVKKKQETRSINEEHTQFLDHLLTGED 536
 QY 481 IVRPLLRLMLTKPHTHYWYRKFDALMR 511
 DB 537 IC-----GHYHHHWK---DKLNR 552

RESULT 13
 157487 Na+ / H+ - exchanging protein, amiloride-sensitive - human
 N;Alternative names: Na+/H+ antiporter; NHE-1
 C;Species: Homo sapiens (man)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 22-Oct-1999
 R;Pieleg, L.; Dyck, J.R.; Wang, H.; Fong, C.; Haworth, R.S.
 Mol. Cell. Biochem. 125, 137-143, 1993
 A;Title: Cloning and analysis of the human myocardial Na+/H+ exchanger.
 A;Reference number: 157487; MUID:94111706; PMID:8283968
 A;Accession: 157487
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-815 <FLI>
 A;Cross-references: GB:S68616; NID:9544775; PIDN: AAC606061; PID:9544776
 R;Zardes, C.; Franchi, A.; Pouysseur, J.
 Cell 56, 271-280, 1989
 A;Title: Molecular cloning, primary structure, and expression of the human growth fac
 A;Reference number: A31311; MUID:89106219; PMID:2536298
 A;Accession: A31311
 A;Molecule type: mRNA

A; Residues: 1-814; 'SNARASRQLSPHLFHQSRCWGLPLPFLTRIGPAPPPTAWOLGPPOPPPQHSSSPAASEASSPPPEL	Qy 89 LPPITFNAGFOVKKKQFPFNFMTITLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVG 146
C; Genetics:	
A; Gene: GDB:SLC9A1; ANNH; NHE1	
A; Cross references: GDB:119683; OMIM:107310	
A; Map position: 1p36.1-1p15	
C; Species: oncorhynchus mykiss (rainbow trout)	
C; Accession: A46188	
R; Borgerse, F.; Saadet, C.; Cappadoro, M.; Pousssegur, J.; Motaïs, R.	
Proc. Natl. Acad. Sci. U.S.A. 89, 6755-6759, 1992	
A; Title: Cloning and expression of a cAMP-activated Na ⁺ /H ⁺ exchanger: evidence that the	
A; Reference number: A46188; PMID:9235712; PMID:1379718	
A; Status: preliminary; not compared with conceptual translation	
A; Molecule type: nucleic acid	
A; Residues: 1-759 <BOR>	
cAMP-activated Na ⁺ /H ⁺ -exchanging protein betaineH - rainbow trout	
C; Species: oncorhynchus mykiss (rainbow trout)	
C; Accession: A46188	
R; Borgerse, F.; Saadet, C.; Cappadoro, M.; Pousssegur, J.; Motaïs, R.	
Proc. Natl. Acad. Sci. U.S.A. 89, 6755-6759, 1992	
A; Title: Cloning and expression of a cAMP-activated Na ⁺ /H ⁺ exchanger: evidence that the	
A; Reference number: A46188; PMID:9235712; PMID:1379718	
A; Status: preliminary; not compared with conceptual translation	
A; Molecule type: nucleic acid	
A; Residues: 1-759 <BOR>	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 31 LIGACTIVS-HLLEE-NFWNNESTALIGCTGTVVILMTPKGSSHLFVESEDLFYI 88	
Db 78 LLALLMKGFHLIPRLSAVVPBSCLLIVGLVGGLIKVGEEPP---VLDSQLEFLCL 133	
Qy 106 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.0%; Score 463; DB: 2; Length 820;	
Best Local Similarity 29.3%; Pred. No. 2.5e-26;	
Matches 138; Conservative 92; Mismatches 187; Indels 54; Gaps 17;	
Qy 48 VNESITALLGLCTVILLMTKGSSHLFVFSEDLFLPPPLIENFGQVKKOPFER 107	
Db 133 VPESCLLIVVGLLGLGLI---KGGETPFLQSQVFFFLPPPLIDAYFLPQFTE 188	
Query Match 16.9%; Score 462; DB: 2; Length 820;	
Best Local Similarity 29.3%; Pred. No. 2.5e-26;	
Matches 138; Conservative 92; Mismatches 187; Indels 54; Gaps 17;	
Qy 80 VNESTALLGLCTVILLMTKGSSHLFVFSEDLFLPPPLIENFGQVKKOPFER 107	
Db 133 VPESCLLIVVGLLGLGLI---KGGETPFLQSQVFFFLPPPLIDAYFLPQFTE 188	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 81 LPPITFNAGFOVKKKQFPFNFMTITLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVG 146	
Db 134 LPPILLDAGYLPIRPFENVGTLVFAVIGLWNANFGGLLYACQIESVGLGVDLL 193	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 147 DFLAIGATFSATDSVCTLQVLNQDE-TFLFLSYLVEGTVNDATSVILFLNALONFLVH 205	
Db 194 ACFLFGSIYSAVDPAVLAVFEEIHINELVHLVGESELNDAVTVVLYNLBEFSKV- 252	
Query Match 17.4%; Score 474; DB: 2; Length 815;	
Best Local Similarity 28.8%; Pred. No. 3.8e-27;	
Matches 146; Conservative 96; Mismatches 203; Indels 62; Gaps 19;	
Qy 18 DYASV---VSNLFLVALCLLACMLKIGPVITPSSVPCCLIVVLLVGLI---KGVS 150	
Db 95 SHLFLVTPFESETWLWLLACMLKIGPVITPSSVPCCLIVVLLVGLI---KGVS 150	
Qy 74 SHLFLVTPFESETWLWLLACMLKIGPVITPSSVPCCLIVVLLVGLI---KGVS 131	
Db 151 ETPPFLQSDVFLFLPPFLDAGYLPLPQTENLGTILFIAVGTLNAAFFGLLMA 210	
Qy 132 IAIFSRMNIGLTDGDFLIAIGAIFSAFDSVCTLQVLNQDE-TFLFLSYLVEGTVNDAT 190	
Db 211 VCLVGGHQINNIGLQDNLFLFSSISAVDPAVLAEHHINELVHLVGESELNDAVI 270	
Qy 191 IFLVFLNQLNF-DLVHIDAVVLFKLGL--NFFYFLSSTFLGVAFLGTLIIVFL 247	
Db 271 VVLYHIEEFANYEH-VGIVDIFLGLFLSPFVVAAGGVYVYVYVYVIAATSR ---FTSH 325	
Qy 248 STDREVALMMIIMAYLSYMAELLDLGSGLTFLVFFCGTVMSHYTWNVNTESRVTKHAFAT 307	
Db 326 IRVIEPLFLYFSYMAVLSAELFLHSIGMALIASGVMPYVEANISHKHTTIKYFLM 385	
Qy 308 LSFAETFLFLYFGMDAIDIE--KNEFASDRPGKSIGTISLIGLVLIGRAAFYFPLSF 364	
Db 386 WSSVSETLIFIFGVSIVVAGSHHWNNTFV-----TISLLE--ECLLARVGLVGLTW 434	
RESULT 15	
A40204	
Na+/H+-exchanging protein 1 - rat	
N; Alternative names: Na ⁺ /H ⁺ -antipporter	
C; Species: Ratios norvegicus (Norway rat)	
C; Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 28-Feb-1997	
C; Accession: A40204	
R; Orłowski, J.; Kandasamy, R.A.; Shull, G.E.	
J. Biol. Chem. 267, 9331-9339, 1992	
A; Title: Molecular cloning of putative members of the Na/H exchanger gene family. cDN	
ally related proteins.	
A; Reference number: A40204; MUID:92250539; PMID:15777624	
A; Accession: A40204	
A; Status: preliminary	
A; Molecule type: mRNA	
A; Residues: 1-820 <ORL>	
A; Cross-references: GB:MB5299	
C; Keywords: transmembrane protein	
Query Match 17.0%; Score 463; DB: 2; Length 820;	
Best Local Similarity 29.3%; Pred. No. 2.5e-26;	
Matches 138; Conservative 92; Mismatches 187; Indels 54; Gaps 17;	
Qy 108 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 16.9%; Score 462; DB: 2; Length 820;	
Best Local Similarity 29.3%; Pred. No. 2.5e-26;	
Matches 138; Conservative 92; Mismatches 187; Indels 54; Gaps 17;	
Qy 109 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 110 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 111 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 112 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 113 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 114 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 115 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 116 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 117 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 118 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 119 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 120 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 121 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 122 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 123 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 124 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 125 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 126 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 127 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 128 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 129 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 130 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 131 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 132 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 133 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 134 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 135 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 136 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 137 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 138 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 139 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 140 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 17.38; Score 472; DB: 2; Length 759;	
Best Local Similarity 28.78; Pred. No. 4.9e-27;	
Matches 140; Conservative 96; Mismatches 188; Indels 64; Gaps 18;	
Qy 141 NFMFTLFGAVGTMISFFTIS--IAIAIAIFSRMNIGTLDVGDFLAIGAFSATSDVCTLQ 165	
Db 189 NLGTLLIFAVGTLNAFFGLLYAVLGGEQINNIGLDTLFGTS1SAVDPAVALA 248	
Query Match 1	

Qy 282 GIVMSHYTWHINVTTESSRVTKHAFATLSFIAETFLFLYVGMDAL-DIEKWEFAASDRPGKS 340
 Db 364 GVVMRPYVEANISHSHTTICKYFLRMWSSVSTLIFIFLGWSTYAGSHONW-----T 416

 Qy 341 IGISSITLLGLVIGRAAFVFFPSLNSNLTKAPNEKITIWROQVITIWAGLMRGAVSTALA 400
 Db 417 FVISTL--FOLIARYLGVLWTWF IN--KFRIYKLTPADQFTIAYGGL-RGATAFSLG 470

 Qy 401 YNKFTRSQHTQLHGNAIMTSITVVLFSITMVEGMNTKPLTRLLPASHPVTSEPPSPK 460
 Db 471 Y--LLDKKKHFMCD--LFELTAITYVIFTVYVQGMTIRPLVDLL----AVKKKQETKR 520

 Qy 461 SLHSPLITSMQGSDLESTTNVRPSSLRMLLTKEPTHTVHYWKRFDDALMR 511
 Db 521 SINEEHTQFIDHLTLTGIEDC-----GHYGHHHWK---DKUNR 556

Search completed: March 26, 2003, 18:54:19
 Job time : 28 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	541	19.9	669	1 NAH6_HUMAN	Q92581 homo sapien
2	533	19.6	633	1 NAH2_YEAST	Q04121 saccharomyces cerevisiae
3	492	18.1	812	1 NAH9_RABBIT	P26432 oryctolagus cuniculus
4	485	17.8	809	1 NAH5_HUMAN	P50482 oryctolagus cuniculus
5	485	17.8	896	1 NAH3_HUMAN	Q14940 homo sapien
6	482.5	17.7	834	1 NAH1_RABBIT	P48764 homo sapien
7	481	17.7	816	1 NAH3_RAT	P23791 oryctolagus cuniculus
8	480.5	17.7	831	1 NAH2_HUMAN	P26433 ratmus norvegicus
9	480	17.6	812	1 NAH3_DIDMA	Q9uby0 homo sapien
10	480	17.6	839	1 NAH2_RAT	P28362 didelphis marsupialis
11	479	17.6	813	1 NAH1_MOUSE	P48763 ratmus norvegicus
12	479	17.6	820	1 NAH1_RAT	Q61165 mus musculus
13	479	17.6	898	1 NAH1_CRIGR	P28036 bos taurus
14	478	17.6	822	1 NAH1_BOVIN	P28762 sus scrofa
15	476	17.5	817	1 NAH1_PIG	P26431 ratmus norvegicus
16	476	17.5	820	1 NAH1_RAT	P19634 homo sapien
17	476	17.5	820	1 NAH1_HUMAN	Q01345 oncorhynchus tshawytscha
18	474	17.4	815	1 NAH2_LNCMV	P26434 ratmus norvegicus
19	472	17.3	759	1 NAH4_RAT	O16452 canenorhabdilis
20	456	16.8	717	1 NAH3_CAEEL	P35449 canenorhabdilis
21	395	14.5	651	1 NAH9_CAEEL	Q50678 mycobacterium tuberculosis
22	390	14.3	667	1 YMF7_MYCTU	P32703 escherichia coli
23	236.5	8.7	542	1 YJCE_ECOLI	P76007 escherichia coli
24	231	8.5	549	1 YCGO_ECOLI	Q42701 zygosaccharomyces pombe
25	186.5	6.9	578	1 YB88_ECOLI	P10502 salmonella enterica
26	159	5.8	808	1 NAH2_ZYGRO	P51648 buchnera apiculata
27	142.5	5.2	426	1 Y057_METJA	P10247 ratmus norvegicus
28	140.5	5.2	791	1 NAH1_ZYGRO	P07117 escherichia coli
29	139.5	5.1	635	1 SL56_HUMAN	P54408 bacillus subtilis
30	138.5	5.1	383	1 NAPA_ENTHR	P34855 apis mellifera
31	137.5	5.1	985	1 NAH1_YEAST	P36606 schizosaccharomyces pombe
32	133.5	4.9	422	1 YF21_METJA	P31077 wolinella sphaeroides
33	131.5	4.8	759	1 NAH2_SCHPO	

Query Match						
Best Local Similarity		Score		Length		
Matches 164; Conservative		541;		669		
FT	TRANSMEM	28	48	POTENTIAL.		
FT	TRANSMEM	71	91	POTENTIAL.		
FT	TRANSMEM	103	123	POTENTIAL.		
FT	TRANSMEM	142	162	POTENTIAL.		
FT	TRANSMEM	179	199	POTENTIAL.		
FT	TRANSMEM	220	240	POTENTIAL.		
FT	TRANSMEM	246	266	POTENTIAL.		
FT	TRANSMEM	292	312	POTENTIAL.		
FT	TRANSMEM	340	360	POTENTIAL.		
FT	TRANSMEM	382	402	POTENTIAL.		
FT	TRANSMEM	404	424	POTENTIAL.		
FT	TRANSMEM	447	467	POTENTIAL.		
SQ	SEQUENCE	483	503	POTENTIAL.		
MW:		741.61	MW:	F6416596229F2639	CRC64;	
Query Match						
Best Local Similarity		19.9%		Score 541;		
Matches 164; Conservative		29.9%; Pred. No. 3.5e-28;		Length 669;		
Qy	1 MGMEVAAARLGALYTTSDSAIVSVINLFLVALCACIYVLGHILEEN - RWVNFSITALLIG 58					
Db	53 MDEBIVSERKQAEEBSHRODSANIL -- IFLILUUTLTITLWFKHRARELYETGLAMIYG 109					
Qy	59 LCTGVV - - - - - ILMTKGKSSH -- LFVFSEDFIYLFLPPLIFENAGFQVK 102					
Db	110 LLGVLRVLRGIHVPSDVNNVNTSCEQSPTTLLVTFDPEVFNLILLPP1FYAGYSLKR 169					
Qy	103 KQPFNFFYLFLSSTFLFGAVTMISFPTISIAAIAFSRMNIGLTVDGVDF - - - LAIGAIFSA 157					
Db	170 RHEFRNLSLLAYAFLGTAISFVGISIMGGVTLNKVTQGADQDYFTDOLLEFAIVSA 229					
Qy	158 TDSVCTLQLVQNQDETPE - LYSLVFGEGVVNDATSIYLFNALQNF - - DLVH - IDAAVL 211					
Db	230 TDPTVTLIAFHBLQDVLEYAIIFLGSEVNLDAVATYLSSSIVAYQPGADSHTFDVTAFL 289					
Qy	212 KFLGNFFYLFLSSTFLFGVAGLISLAVYIJK - KLYIGRHSIDREVALMLMAYLSYMLAEI 269					
Db	290 KSGIIFLGFCSFANGAATGATVYTAFLVKTFLK - - REFPQLETLGFLFMSWSFLAEEA 346					
Qy	270 LDLSGLLTIVFCGYMVAHLVHNVTESSRPTKHAFATLSTAETFLFLYGMDALDIEK 329					
Db	347 WGFTGVVAVFLCGITQAHYTTNNLSTESQRTKQLFELLNLAENEFYSMGLLTFLFTON 406					
Qy	330 WEFASDRPGKSIGISSILGLVLIGRAAFYFPFLSPLSNLTKAPNEKITWQRQQVIVWAG 389					
Db	407 HVF -- NPTPVVG - - - AFAIFIQLGRAANIPYPLSLNNGRRS -- KTGNSNEQHMMMPAG 456					
Qy	390 LMRGAVSIALAYNKPLTRSGHTQLQIGNAINTSTIVVLFSTMYPGMMTKPLIRLULLPASG 449					
Db	457 L - RGAMAFAAIR - - - DATVAFAROMFESTLILIVFPTVWYFGGTATMLSQL - - - 504					
Qy	450 HPVTESEPSSPKSLHSPLTSMQSDLESTNVRPSSLRMLLTKPHTVHYWWRKEDDAL 509					
Db	505 HIRGVYDSDOEHLGVP - - - ENERRTTKAEEAWLPRM - - - - - WYNFDHNY 545					
Qy	510 MRPMFGRG 518					
Db	546 LKPLLTMSG 554					

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Db 293 IESCLLIILATESYFFNSGCHMSIVSLFCGITLKHYAYNMRSQITIKYTFQLLAR 352
    |::|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Db 311 IAETELFLYVGNDAL-DIEKKEFASDRPGKSIGISSLGLI---VLIGHAAFEPLS-- 363
    ::|:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Qy 353 LSENFIFTYGLIEFLFTEVE-----LVYKPLLTVVAISCVARWCAPLSQF 400
    :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Db 364 -----FSLNLNTK--APNEKTTWQRQQVVIWAGLMLRGAVSIALAYN----KF 404
    :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Qy 405 TRSGHTOLHGNAIMTSTITYVLFSTMFGNMKTPLIRLILPASHGPVTPSPSK--SL 462
    :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Db 459 T-----LLATLVVVVLTFLFGTTAGMLEVNLNIKG-CISEEDTSDDDEFDI 505
    :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Db 463 HSP-LLTSMOGSDE-----STT----- 479
    :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Db 506 EAIPRAINLNGSSITQDGPYSDNNSPDISTQFAVSSNKNLPNNSTGGNTFGGLNET 565
    :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Qy 480 -----NIVRPS-----SLRMLLTKPKTHVYYWRKFDDALMRPMF 514
    :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|
Qy 566 ENTPSPNPARRSSMDKRNLRDKLTIFNSDQNQNEDQVLRKPVF 609
    :||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:|

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RESULT 3
ID NAH3_RABIT STANDARD; PRT; 832 AA.

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AC P24342;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 25-JUN-2002 (Rel. 41, Last annotation update)
DT Sodium/hydrogen exchanger 3 (Na(+)/H(+) exchanger 3) (NHE-3).
GN SLC2A3 OR NHE3.
OS Oryctolagus cuniculus (Rabbit).
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TAXID=9386;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=New Zealand White; TISSUE=ileal villus, and kidney cortex;
RX PubMed=13744392;
RA Tse C.-M., Brant S.R., Walker S.S., Pouyssegur J., Donowitz M. ;
RT Cloning and sequencing of a rabbit cDNA encoding an intestinal and
kidney-specific Na+/H+ exchanger isoform (NHE-3).";
RL J. Biol. Chem. 267:9340-9346 (1992).
CC - FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
TRANSDUCTION.
CC - SUBCELLULAR LOCATION: Integral membrane protein.
CC - TISSUE SPECIFICITY: INTESTINAL AND KIDNEY SPECIFIC. MOST ABUNDANT
IN KIDNEY CORTEX, FOLLOWED EQUALLY BY ILEUM AND ASCENDING COLON,
THEN KIDNEY MEDULLA AND JEJUNUM. IS ABSENT FROM DUODENUM AND
DESCENDING COLON.
CC - PTM: PHOSPHORYLATED (POSSIBLE).
CC - SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CC - CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.

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PRINTS; PRO1084; NAHEXCHNGR;
DR TIGR00840; b_cpal; Transport; Antiprot; Sodium transport;
DR Transmembrane; Glycoprotein; Transport; Antiprot; Sodium transport;
KW Multigene family; Phosphorylation; CYTOPLASMIC (POTENTIAL).
FT DOMAIN 1 11
FT TRANSEM 12 27
FT DOMAIN 28 59
FT TRANSEM 60 79
FT DOMAIN 80 81
FT TRANSEM 82 101
FT DOMAIN 102 110
FT TRANSEM 111 130
FT DOMAIN 131 134
FT TRANSEM 135 154
FT DOMAIN 155 180
FT TRANSEM 181 200
FT DOMAIN 201 209
FT TRANSEM 210 229
FT DOMAIN 230 250
FT TRANSEM 250 269
FT DOMAIN 270 298
FT TRANSEM 299 319
FT DOMAIN 320 339
FT TRANSEM 340 359
FT DOMAIN 360 366
FT TRANSEM 367 385
FT DOMAIN 386 435
FT TRANSEM 436 455
FT DOMAIN 456 832
FT CARBOHYD 325 325
FT VARIANT 144 144
SQ SEQUENCE 832 AA; Score 492; DB 1; Length 832;
Query Match 18.18%; Best Local Similarity 31.34%; Pred. No. 6.9e-35; Matches 143; Conservative 91; Mismatches 171; Indels 52; Gaps 18;
OY 25 INLFVALLCACIVLGHLLEE-NRWYNESITALIIGLCTGVVILMLTKGKSSH-L-FVFSSE 81
DB 57 IALWLVVASLAKIVFHLSKIVTWSPEVDSLVLVGLGVV----ADHIASFSTLP 111
OY 82 DLFFIYLLPPLFLFNAGFOVKKQKFRRNEMTFLFGAVGTGMISFFFTISIAIAIFSRMNING 141
DB 112 TVFFFYLLPLVLDAGFMPNRLFMSLGSLLIAVVGTVWNAATFGTLSLYGVFSLSIMG 171
OY 142 TLDVG-DFLGAISATSDVCTLQVLNQ-DTEPFLSVEGEVWNTDSVTLFNLQ 198
DB 172 ELKIGLIDFLFGSLLAADVDPAVLVFEEHVNVNLFIVGESLINDAVTVVNVFQ 231
OY 199 NFDLVHDAAV--VLFKLGNNPFYLFLSFLFG-VFAGLISAYIKKLYGRHSTDREVA 254
DB 232 SVTLCGDKVTVGDCVKIVSFVSVGGTLYVPAFLS--IVTR-FTKHYVIEPG 287
OY 255 LMMLMAYLSYMLAEDLDSLGTFLVCGTMSHYTVVNTBESSRVTKHAFATLSIAET 314
DB 288 FVFTISLYSLTSEMLSLSSIIATFGCICOKYKANISEQSATVRYTHKMLASGAET 347
OY 315 FFLYVGMDALDEKWEFASDRPGKSIGISSLGLVILIG--RAAFYFPLSLSNLTKKA 372
DB 348 LIIFMFLGTSADPLINTW-----NTAFVLTLLFVSVERAIGVYQFWLNNRYRMV 398
OY 373 PNEKTIWQRQVVIWAGLMLRGAVSIALAYNKTRSGHTQLHGNIA---MITSTITVVLF 428
DB 399 QEI I - DQVWMSYGLL-RGAVAEALV-----ALLJSNKVKKEKNFVSTTIVF 445
OY 429 STMVF-GMMTKPLIR-LILLPASGHPVTESEPPSPKSLH 463
DB 446 FTVFQGLTIPQWLKVKRSEH--REPKLNEKLH 479

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RESULT 4
NAH2_RABIT
ID NAH2_RABIT STANDARD; PRT; 809 AA.

AC P50482;	FT TRANSMEM	459	479	M (M1) (POTENTIAL).
DT 01-OCT-1996 (Rel. 34, Created)	FT DOMAIN	480	809	CYTOPLASMIC (POTENTIAL).
DT 01-OCT-1996 (Rel. 34, Last sequence update)	FT CARBOHYD	350	350	N-LINKED (GLCNAC (POTENTIAL)).
DT 15-JUN-2002 (Rel. 41, Last annotation update)	FT SEQUENCE	809	AA:	DBD00B45443D87A6 CRC64;
DE Sodium/hydrogen exchanger 2 (Na(+)/H(+) exchanger 2) (NHE-2).				
GN SLC9A2 OR NHE2.				
OS Oryctolagus cuniculus (Rabbit).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;				
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
OX NCBI_TaxID=9986;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=New Zealand white.				
RA MEDLINE=93280159; PubMed=7685025;				
RA Tse C.-M., Levine S.A., Yun C.H., Montrose M.H., Little P.J.,				
RA Donowitz M.;				
RA Cloning and expression of a rabbit cDNA encoding a serum-activated				
RT ethylisopropylamiloride-resistant epithelial Na+/H+ exchanger isoform				
RT (NHE-2).";				
RL J. Biol. Chem. 268:11917-11924 (1993).				
CC -!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED				
CC BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL				
CC CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD				
CC SODIUM ION CHEMICAL GRADIENT. SEEKS TO PLAY AN IMPORTANT ROLE IN				
CC COLONIC SODIUM ABSORPTION.				
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.				
CC -!- TISSUE SPECIFICITY: HIGH LEVELS IN INTESTINE AND KIDNEY.				
CC -!- PTM: PHOSPHORYLATION (POSSIBLE).				
CC -!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.				
CC -!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC				
CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.				
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CC -!- -!- EMBL; L13733; ; NOT_ANNOTATED_QDS.				
DR InterPro; IPR00676; NAH_Exchnt.				
DR InterPro; IPR004709; NAH_exchang3.				
DR Pfam; PF00999; Na_H_Exchanger_1.				
DR TIGRFAMS; TIGR00840; NAH2XCHNRE.				
KW Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport;				
KW Multidene family; Phosphorylation.				
FT DOMAIN 1 16 CYTOPLASMIC (POTENTIAL).				
FT TRANSMEM 17 37 A (M1) (POTENTIAL).				
FT DOMAIN 38 79 CYTOPLASMIC (POTENTIAL).				
FT TRANSMEM 80 100 B (M2) (POTENTIAL).				
FT DOMAIN 101 106 CYTOPLASMIC (POTENTIAL).				
FT TRANSMEM 107 127 C (M3) (POTENTIAL).				
FT DOMAIN 128 138 EXTRACELLULAR (POTENTIAL).				
FT TRANSMEM 139 159 D (M4) (POTENTIAL).				
FT DOMAIN 160 168 CYTOPLASMIC (POTENTIAL).				
FT TRANSMEM 169 189 E (M5) (POTENTIAL).				
FT DOMAIN 190 208 EXTRACELLULAR (POTENTIAL).				
FT TRANSMEM 209 229 F (M5A) (POTENTIAL).				
FT DOMAIN 230 236 G (M5B) (POTENTIAL).				
FT TRANSMEM 237 257 EXTRACELLULAR (POTENTIAL).				
FT DOMAIN 258 277 J (M8) (POTENTIAL).				
FT TRANSMEM 278 298 K (M9) (POTENTIAL).				
FT DOMAIN 299 307 CYTOPLASMIC (POTENTIAL).				
FT TRANSMEM 308 328 I (M7) (POTENTIAL).				
FT DOMAIN 329 360 EXTRACELLULAR (POTENTIAL).				
FT TRANSMEM 361 381 J (M8) (POTENTIAL).				
FT DOMAIN 382 391 CYTOPLASMIC (POTENTIAL).				
FT TRANSMEM 392 412 K (M9) (POTENTIAL).				
FT DOMAIN 413 429 EXTRACELLULAR (POTENTIAL).				
FT TRANSMEM 430 450 L (M10) (POTENTIAL).				
FT DOMAIN 451 458 EXTRACELLULAR (POTENTIAL).				
	RESULT 5			
	NAH5_HUMAN			
ID NAH5_HUMAN STANDARD				
AC Q14940; Q9Y626;				
DT 01-NOV-1997 (Rel. 35, Created)				
DT 16-OCT-2001 (Rel. 40, Last sequence update)				
DT 15-JUN-2002 (Rel. 41, Last annotation update)				
DE Sodium/hydrogen exchanger 5 (Na(+)/H(+) exchanger 5) (NHE-5).				
GN SLC9A5 OR NHE5.				
OS Homo sapiens (Human).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX NCBI_TaxID=9606;				
RN [1]				
RC SEQUENCE FROM N.A.				
RA TISSUE=Brain;				
RA MEDLINE=99134372; PubMed=9933641;				
RA MEDLINE=95178929; PubMed=7759094;				
RA "Molecular cloning, genomic organization, and functional expression of				
RA Na+/H+ exchanger isoform 5 (NHE5) from human brain.".				
RL J. Biol. Chem. 274:4377-4382 (1999).				
RN [2]				
RD SEQUENCE OF 64-218 FROM N.A.				
RX MEDLINE=95178929; PubMed=7759094;				
RA Klanké C.A., Su Y.R., Callen D.F., Meneton P., Baird N.,				
RA Kandasamy R.A., Orlowski J., Otterud B.E., Leppert M., Shull G.E.,				

FT	DOMAIN	54	CYTOPLASMIC (POTENTIAL).	DE	Sodium/hydrogen exchanger 1 (Na(+)/H(+) exchanger 1) (NHE-1).
FT	DOMAIN	73	B (M2) HYDROPHOBIC.	GN	SLC9A1 OR NHE1.
FT	TRANSEM	74	CYTOPLASMIC (POTENTIAL).	OS	Oryctolagus cuniculus (Rabbit).
FT	TRANSEM	80	C (M3) (POTENTIAL).	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
FT	TRANSEM	100	EXTRACELLULAR (POTENTIAL).	OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
FT	TRANSEM	112	D (M4) (POTENTIAL).	OX	NCBI_TaxID=9867;
FT	TRANSEM	113	CYTOPLASMIC (POTENTIAL).	RN	[1]
FT	TRANSEM	134	E (M5) (POTENTIAL).	RP	SEQUENCE FROM N.A.
FT	TRANSEM	140	EXTRACELLULAR (POTENTIAL).	RC	STRAIN=New Zealand white; TISSUE=Ileal villus;
FT	TRANSEM	161	F (M5A) (POTENTIAL).	RX	Medline=91293066; PubMed=1712287;
FT	TRANSEM	181	CYTOPLASMIC (POTENTIAL).	RA	Ts C.-M., Ma A.-J., Yang V.W., Watson A.J.M., Levine S.,
FT	TRANSEM	203	G (M5B) (POTENTIAL).	RA	Montrose M.H., Potter J., Sardet C., Pouyssegur J., Donowitz M.;
FT	TRANSEM	211	EXTRACELLULAR (POTENTIAL).	RT	"Molecular cloning and expression of a cDNA encoding the rabbit ileal
FT	TRANSEM	233	H (M6) (POTENTIAL).	RT	villus cell basolateral membrane Na+/H+ exchanger.";
FT	TRANSEM	253	CYTOPLASMIC (POTENTIAL).	RL	EMBO J. 10:1957-1967(1991).
FT	DOMAIN	275	I (M7) (POTENTIAL).	RN	[2]
FT	TRANSEM	291	EXTRACELLULAR (POTENTIAL).	RP	SEQUENCE FROM N.A.
FT	DOMAIN	310	J (M8) (POTENTIAL).	RC	TISSUE=Kidney;
FT	TRANSEM	341	CYTOPLASMIC (POTENTIAL).	RX	Medline=9206447; PubMed=1661611;
FT	TRANSEM	363	K (M9) (POTENTIAL).	RA	Hildebrandt F., Pizzonia J.H., Reilly R.F., Reboucas N.A.,
FT	TRANSEM	370	EXTRACELLULAR (POTENTIAL).	RA	Sardet C., Pouyssegur J., Slayman C.W., Aronson P.S., Igashii P.;
FT	DOMAIN	391	L, HYDROPHOBIC.	RT	"Cloning, sequence, and tissue distribution of a rabbit renal Na+/H+
FT	DOMAIN	406	EXTRACELLULAR (POTENTIAL).	RT	exchanger transcript.";
FT	TRANSEM	427	M (M10) (POTENTIAL).	RL	Biochim. Biophys. Acta 1129:105-108(1991).
FT	TRANSEM	436	EXTRACELLULAR (POTENTIAL).	RN	[3]
FT	TRANSEM	456	CYTOSMIC (POTENTIAL).	RP	SEQUENCE OF 472-816 FROM N.A.
FT	CARBOHYD	834	N-LINKED (GLCNAC . . .) (POTENTIAL).	RC	STRAIN=New Zealand white; TISSUE=Heart muscle;
FT	CARBOHYD	326	N-LINKED (GLCNAC . . .) (POTENTIAL).	RX	Medline=91138752; PubMed=1704856;
SQ	SEQUENCE	834 AA:	92907 MW: 37ECE33D65DF7 CRC64;	RA	*Identified L., Sardet C., Pouyssegur J., Barr A.;
Query Match		17 7%	Score 482.5; DB 1; Length 834;	RT	"Identification of the protein and cDNA of the cardiac Na+/H+
Best Local Similarity		31.4%	Pred. No. 2.9e-24; Mismatches 158; Indels 51; Gaps 17;	RL	FEBS Lett. 279:25-29(1991).
Matches 136: Conservative		88		CC	-!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
QY	48	VNESTALIGLCTGVILLMTKRSQSHL--FVFSSEDDIFFYLPLPFITNAFLGQVKRKFQF 105		CC	BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
Db	82	VPESSLIVLVLGGIV-- --WAADHIASTFLTPTVFFYLPLPVTDAGYFMPNLF 116		CC	CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
QY	106	PRNFMTITLEAVGAVTMISFTISIAIAIFSRMNTGTLDVG--DFAIAGAIFSATDSVCT 163		CC	SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
Db	137	FGNUTLILAYGTGTVWATGSLYGLYFSLGMQDQIGLNLFLFGSLMAVDPAV 196		CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.
QY	164	LOVING--DTPFLYSLVGFYNDATVFLNALQNDLV--HIDAAYVVLKFLGNFFY 219		CC	-!- TISSUE SPECIFICITY: KIDNEY AND INTESTINE.
Db	197	LAFFEEHVNEVLFITVGESSLNDAVTVLYNVFESVAGDNVITGVDVGIVSFV 256		CC	CC -!- PTM: PHOSPHORYLATED (POSSIBLE).
QY	220	LFLSSTFLG-VFAGLSSAYIUKKLYIGRHSTDREVALMMAYLSYMLAELLDLSGLTV 278		CC	CC -!- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
Db	257	VSGGTTLNGVVFAPLLS--LTVR--FTTHVRLIEPGFWLISYLSYLTSEMISLSATLAI 312		CC	CC -!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
QY	279	FEGGIVMSHTWINTVTESSRTTKHAFATLSFAETFLFLYGMDALIEKKFEASDRPG 338		CC	CC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
Db	313	TFCGCCCCCKYKANISQSATVYTMKMLASSAETLIMFGISANPFTWW----- 366		CC	CC -----
QY	339	KSIGISSLGLLGVLG--RAAVVPLSPLSLNLTJKAPNEKTIWQOQVVIWAGLMGAVS 396		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
Db	367	--NTAFVFLTLYFISVYRAIGVLTQFLWLNRYMOLEPI--DQVFLSTGGL-ROAVA 419		CC	CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
QY	397	IALAYNKFTRSGHTQHGNAT---MITSTITVVLFESTMVF-GMMTKPLIR-LILLPASGH 450		CC	CC the European Bioinformatics Institute. There are no restrictions on its
Db	420	PAV-----VLLDDGDKVKEKNLNFVSTTIVVFTVIFQGLTIPKVKRSEH 470		CC	CC use by non profit institutions as long as its content is in no way
QY	451	PVTEPPSSPKSLH 463		CC	CC modified and this statement is not removed. Usage by and for commercial
Db	471	--REPRINEKHL 480		CC	CC entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RESULT 7				CC	CC -----
ID	NAH1_RABBIT		STANDARD;	DR	EMBL: X59935; CAA2558; 1; -;
AC	P23791;		PRT;	DR	EMBL: X61504; CAA43721; 1; -;
DT	01-NOV-1991	(Rel. 20)		DR	EMBL: X56536; CAA39881; 1; -;
DT	01-NOV-1991	(Rel. 20)	Last sequence update	DR	PRINTS; PRO1084; NA_H_Exchanger; 1.
DT	15-JUN-2002	(Rel. 41)	Last annotation update	DR	TIGRFAMs; TIGR00840; b_cpal; 1.
				DR	Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport;
				KW	Multigene family; Phosphorylation.
				FT	CYTOPLASMIC (POTENTIAL).
				FT	M1 (POTENTIAL).
				FT	TRANSMEM
				FT	TRANSMEM
				FT	M2 (POTENTIAL).
				FT	TRANSMEM
				FT	M3 (POTENTIAL).
				FT	TRANSMEM
				FT	TRANSMEM
				FT	TRANSMEM

Query Match 17.7%; Score 480.5; DB 1; Length 831;
 Best Local Similarity 28.6%; Pred. No. 3.8e+24;
 Matches 146; Conservative 101; Mismatches 197; Indels 67; Gaps 19;

Qy 22 VVSNLFVALSLCACIV-LGHILLEENRGYNESTIALLGLCTGVVTLMTKGSSHL -FV 78
 Db 54 ITALWILWASLAKIIVEFHISH -- KVTSVTPESALLIVLGLVGIV ---WAADHIASET 106
 Qy 79 FSEDLFFTYLLPPIFLIENAGFQVKKKQPFERNFMITLFGAVGMISFFTISAAIAIFSRM 138
 Db 107 LPLTLEPPYLPLPPIVLDAYGMPNRLFFGNLGTLLYAVIGTIWNAATTGSLSYGFPLSG 166
 Qy 139 NIGTLDVG -DEFLAIGAIFSATDSVQLVNQ -DFTPLFLSVLVEGVVNDATSIYLFN 195
 Db 167 LMGELKIGLIDELFLGSIIIAVDPVAVLAEFEHVNEVLFLIVFGESLNDLDAVTWLYN 226
 Qy 196 ALQNFDLVHTDAV -- -VLFKLFGNNFYLFLESSLSTFLGV -FAGLSSAYLIKKLYIGRHSTD R 251
 Db 227 VFSFVTLGGDAVTGVDCKVGIVSFFVVSLSGTLVVEFIAFLS -- LVTR -FTKVRII 282
 Qy 252 EVAFLMMIAYLMSYMLAFLDLSGLTIVFCCGIVMSHYTWNNVTESSRVTKHAFATLSFI 311
 Db 283 EPGFVVISYLSYLTSMSLMSLSSAIIATCQGCCQYKVANISEQATTVRYTMKMLASG 342
 Qy 312 AETFLFLYVGMDALDLEKWEASDRDGKSIGISSILGLLIG -- RAAFVPLSFLSNL T 369
 Db 343 AETIIMFLGISAVIDPVITWV -----NTAFVFLTLVLSIVSYRAIGVVLQTLWLNRY 393
 Qy 370 KKPANEKITWROQQVITIWAGLMRGAWSIALAYNKTFIRSQTQHLGRNAIMITSTIVLVS 429
 Db 394 RMYOLETI -- DQVNSYGGL -RGAVAYALV -- -VLLDEKKVKVEKNLIVFT 445
 Qy 430 TMVFGMTKPLIRLTLPA5GHPVTSEPPSPPSLH --- SPLITSMGSDLESTTNIVRPS 485
 Db 446 VIFQGTTIKPLVQWLKVKRSE -- QREPKLNKLRGAFDHILLSAIEDISQIGHNYLRDK 503
 Qy 486 SLRMLLTKPTVHYWKRFD -- -DALMR 511
 Db 504 ----- WSNFRKFLSKVLMR 518

RESULT 9

NAH2_HUMAN STANDARD; PRT; 812 AA.
 ID NAH2_HUMAN
 AC Q9UBY0;
 DT 16-OCT-2001 (Rel: 40, Created)
 DT 15-JUN-2002 (Rel: 40, Last sequence update)
 DE Sodium/hydrogen exchanger 2 (Na⁽⁺⁾/H⁽⁺⁾ exchanger 2) (NHE-2).
 GN NHE2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1] RN MEDLINE=90375108; PubMed=1044453;
 RN NCBI_TAXID=9606;
 RN SEQUENCE FROM N.A.

RC RX

RAMAKOTTO J., DAHDAL R.Y., SCHMIDT L., LAYDEN T.J., DUDEJA P.K.,
 RAMASWAMY K.; "Molecular cloning, tissue distribution, and functional expression of
 the human Na⁽⁺⁾/H⁽⁺⁾ exchanger NHE2.";
 Am. J. Physiol. [2] 277:G383-G390(1999).

SEQUENCE FROM N.A.

HOU S., WOHLHORST P.

Submitted (APR 1999) to the EMBL/GenBank/DBJ databases.

RT "Functional cloning, tissue distribution, and functional expression of
 the human Na⁽⁺⁾/H⁽⁺⁾ exchanger NHE2.";
 RL Am. J. Physiol. [2] 277:G383-G390(1999).

SEQUENCE FROM N.A.

RA

RA

RA

RA

RA

RA

CC -!- TISSUE SPECIFICITY: EXPRESSED IN SKELETAL MUSCLE, COLON AND
 CC KIDNEY. LOWER LEVELS IN THE TESTIS, PROSTATE, OVARY, AND SMALL
 CC INTESTINE.
 CC -!- PTM: PHOSPHORYLATED (POSSIBLE).
 CC -!- SIMILARITY: BELONGS TO THE NA⁽⁺⁾/H⁽⁺⁾ EXCHANGER FAMILY.
 CC -!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
 CC DOMAINS IN THE NA⁽⁺⁾/H⁽⁺⁾ EXCHANGERS VARY AMONG AUTHORS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC use by non profit institutions as long as its content is in no way
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 CC
 CC DR AF073299; AAD41635.1; -.
 CC DR EMBL; AC007339; AAF19248.1; -.
 CC DR GENBANK; HGNC-11072; SLC9A2.
 CC DR InterPro; IPR000676; NAH_Exchng.
 CC DR InterPro; IPR004709; NAH_Exchng3.
 CC DR PRO0959; NA_H_Exchng; I.
 CC DR PRINETS; PRO084; NAHECHNGR.
 CC DR TIGR00840; b_cpal; 1.
 KW Multigene family; Glycoprotein; Transport; Antiport; Sodium transport;
 KW Multigene family; Phosphorylation.
 FT DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 1 14 A (M1) HYDROPHOBIC.
 FT DOMAIN 34 79 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 80 100 B (M2) HYDROPHOBIC.
 FT DOMAIN 101 106 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 107 127 C (M3) (POTENTIAL).
 FT DOMAIN 128 138 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 139 159 D (M4) (POTENTIAL).
 FT DOMAIN 160 168 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 169 189 E (M5) (POTENTIAL).
 FT DOMAIN 190 208 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 209 229 F (M5A) (POTENTIAL).
 FT DOMAIN 230 236 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 237 257 G (M5B) (POTENTIAL).
 FT DOMAIN 258 277 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 278 298 H (M6) (POTENTIAL).
 FT DOMAIN 299 307 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 308 328 I (M7) (POTENTIAL).
 FT DOMAIN 329 360 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 361 381 J (M8) (POTENTIAL).
 FT DOMAIN 382 391 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 392 412 K (M9) (POTENTIAL).
 FT DOMAIN 413 429 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 430 450 L, HYDROPHOBIC.
 FT DOMAIN 451 458 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 459 479 M13 (POTENTIAL).
 FT DOMAIN 480 812 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 812 AA; 91519 MW; 177E17DC383000A CRC64;

Query Match 17.6%; Score 480; DB 1; Leng 812;
 Best Local Similarity 27.3%; Pred. No. 4e-24;
 Matches 143; Conservative 98; Mismatches 203; Indels 80; Gaps 19;

Qy 16 TSDYAVS -- VSNLFLVALICATVLGHLEE-NRWNESTITALIIGLCTGVVILLMTKG 71
 Db 72 TLDYPHQVQIPPEITLWILLASLAKGFHLTHKLPTIVPESCLLIVGLLGGI1PGVDE-
 Qy 72 KSSHIFVFSEDFLFFYLPLPTIFNAGFQVKKQKFRRNFMITLFGAVGMISFTTISAA 131
 Db 131 KSPP -AMKTDVFFLPLPVILAGYFPTTRPENIGIWFAWVGLWNNSIGGVNL 188
 Qy 132 IAFSRMNIGTLDVG -DELAIGAIFSASTDVCLQLV NQDETPFLSLVFGGVVNDIA 188
 Db 189 FGICQIEAFLGLSDITLQNLLFGSLISAVDPVAVLAVENHNEQLTLYVGESELNDIA 248
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

189	TSTIVLNALQNF-DLVHDAAVYLKFQGNEYFLFLLSSTFLGVAGLISAY-----I	238
y	:: :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :	:
b	249 VTVLYNLFKSFQMKTTETIDVAGIANFFVVGIGGLYIFLGFIAAFTTRFHNRIV	308
b		
239	IKKLYGRHSTDREVALMMLAYLSYMAELLDLSGILTVFFCGIVMSHYTWHNTESSR	298
y	:: :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :	:
b	309 IEPLFV-----FLYSLSYITAEMPHLSGMAITACAMMKYVNEENNSOKSY	356
b		
299	VTRHAFATLSELAEFLFLYVMDAL-DIEKWFEDASDRPGKSIGISSILGLVLIGRAA	357
y	:: :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :	:
b	357 TTIKYFMMQLSSVSETLIFMGYSTVGKHNHEWWA-----FVCFTLAFCLMRRL	407
b		
358	EVFPLSFLSNLTKKAPNEKITWTRQQVYIWAGLMRGAVSIALAY---NKFRSGHTQLH	413
y	:: :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :	:
b	408 GVFVLTQVNRFRTIP---LTFKDQFLTAYGGP-----RGAICFAFLVFLDAAEFR-	456
b		
414	GNAUMITSITVVFLSTWFGMTKPLIRLPLPSAGHPTVSESPSPKLHSPLTSMOGS	473
y	:: :: : :: : :: : :: : :: : :: : :: : :: : :: : :: : :: :	:
b	457 -KKLFITRAIVVIFTVFELGITIRPLVFLDVKRSN--KKQOAVSESIYCRFLDHVK-T	512
b		

RESULT 10			
D NAH3_DIDMA	STANDARD;	PRT;	839 AA.
D NAH3_DIDMA			
C Q2836;			
T 01-NOV-1997 (Rel. 35, Created)			
T 01-NOV-1997 (Rel. 35, Last sequence update)			
T 15-JUN-2002 (Rel. 41, Last annotation update)			
DT Sodium/hydrogen exchanger 3 (Na(+)/H(+) exchanger 3) (NHE-3).			
SLC9A3 OR NHE3			
NN Didelphis marsupialis virginiana (North American opossum).			
NN Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
NN Mammalia; Metazoa; Chordata; Didelphimorphia; Didelphidae; Didelphis.			
NN NCBI_Taxid=9267;			
NN [1]			
NN SEQUENCE FROM N_A.			
NN MEDLINE=93538236; PubMed=7631739;			
NN Amemiya M., Yamaji Y., Cano A., Moe O.W., Alpern R.J.;			
NN "Acid incubation increases NFE-3 mRNA abundance in OKP cells.";			
NN Am. J. Physiol. 269.C126-C133(1995).			
-I- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED			
-I- BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL			
-I- CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD			
-I- SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL			
-I- TRANSDUCTION.			
-I- SUBCELLULAR LOCATION: Integral membrane protein.			
-I- PTM: PHOSPHORYLATION (POSSIBLE).			
-I- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY			
-I- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC			
-I- DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.			

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or send an email to license@isb-sib.ch .			

EMBL; L42522; AAA98816.1; -			
InterPro; IPR000676; NaH_Exchngr3.			
InterPro; IPR00470; NaH_Exchng3.			
Pfam; PF00939; Na_H_Exchanger_1.			
PRINTS; PR01084; NAHExchNGR.			
TIGRFams; TIGR00840; b_cpa1; 1.			
Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport;			
Multigene family; Phosphorylation.			
DOMAIN 1 13 CYTOPLASMIC (POTENTIAL).			
TRANSMEM 14 31 M1 (POTENTIAL).			

	RESULT	11
NAH2_RAT	NAH2_RAT	STANDARD;
ID	NAH2_RAT	PT;
AC	P48765; Q16434;	813 AA.
DT	01-FEB-1986 (Rel. 33, Created)	
DT	01-FEB-1986 (Rel. 33, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
DE	Sodium/hydrogen exchanger 2 (Na(+) / H(+)) exchanger 2 (NHE-2)	
GN	SLC9A2 OR NHE2.	
OS	Rattus norvegicus (Rat).	
Query Match	22 VVSINFLVALLCACTV LGHLLEENKVNNESTALIGLCTGVVLLMLTGKGSQHLL	Score 480; DB 1; Length 839;
Best Local Similarity	30.3%	Pred. No. 4 2e-24;
Matches	138; Conservative 94; Mismatches 179; Indels 44	
Qy	79 FSEDFLEFLYLLPPIFNFQVKKOPFRNEMTITLGAVGTMISFTTISIAAI	
Db	115 LPTVFFYLLPPIVLDAGYFPNPRLFFGNLTILLYAVIGTVWWAAATTGLSILVG	
Qy	139 NIGHTDVG -DFLAGIAFLSATSVDCTQLQVLNQ -DETPFLYSLVFGEGVYNDATSI	
Db	175 IMGDLSIGLDFJFGSLLIAADPVAVLAVEEHVNDVLFLIVGESLUNDAYTV	
Qy	196 ALQNFDLPHIDAAV - -VLFKEGFNFYFLSLSTEFLG-VFAGLISAYIILKLYIGHH	
Db	235 VFDSDFLGPVTDGKVTGDCVQGIVTSVSLGTLGTTGIAFLS - LVTR - FTHW	
Qy	252 EVALMMIIMAYLSVMAELLDLSLITVFFPGVLMSHYTWHNVTESSRVTKHAFAT	
Db	291 EPGVVFISLYSITSEMISLSIALTFCGICQCQYKANISEQGATTVRTYTMK	
Qy	312 AETFLFLYVGMDALDIKEWEFASDRPGKSIGISSIIILGLVLIG --RAAFYEPPLSF	
Db	351 AETIFMFLGISAVIDPAITWT - - - - -NTAFILELTLVFLSVYRAIGVVQLTWI	
Qy	370 KKAENKEITWROQVTTWAGLMLGAVALAANKFRTSGHTQLHGNAIMTISTTIV	
Db	402 RMVQLEIIT - -DQVMSYGLG - RGAVAYALV - - -VLLDEKRVKEKNLFVSTTIV	
Qy	430 TMVFGMMTKPLIR - LILLPASGHPVTEPSSPKSLH 463	
Db	454 VIFQGLTIRPLVQWLKVKSEH - - -REPKLNEKLH 485	
Query Match	22 VVSINFLVALLCACTV LGHLLEENKVNNESTALIGLCTGVVLLMLTGKGSQHLL	Score 480; DB 1; Length 839;
Best Local Similarity	30.3%	Pred. No. 4 2e-24;
Matches	138; Conservative 94; Mismatches 179; Indels 44	
Qy	79 FSEDFLEFLYLLPPIFNFQVKKOPFRNEMTITLGAVGTMISFTTISIAAI	
Db	115 LPTVFFYLLPPIVLDAGYFPNPRLFFGNLTILLYAVIGTVWWAAATTGLSILVG	
Qy	139 NIGHTDVG -DFLAGIAFLSATSVDCTQLQVLNQ -DETPFLYSLVFGEGVYNDATSI	
Db	175 IMGDLSIGLDFJFGSLLIAADPVAVLAVEEHVNDVLFLIVGESLUNDAYTV	
Qy	196 ALQNFDLPHIDAAV - -VLFKEGFNFYFLSLSTEFLG-VFAGLISAYIILKLYIGHH	
Db	235 VFDSDFLGPVTDGKVTGDCVQGIVTSVSLGTLGTTGIAFLS - LVTR - FTHW	
Qy	252 EVALMMIIMAYLSVMAELLDLSLITVFFPGVLMSHYTWHNVTESSRVTKHAFAT	
Db	291 EPGVVFISLYSITSEMISLSIALTFCGICQCQYKANISEQGATTVRTYTMK	
Qy	312 AETFLFLYVGMDALDIKEWEFASDRPGKSIGISSIIILGLVLIG --RAAFYEPPLSF	
Db	351 AETIFMFLGISAVIDPAITWT - - - - -NTAFILELTLVFLSVYRAIGVVQLTWI	
Qy	370 KKAENKEITWROQVTTWAGLMLGAVALAANKFRTSGHTQLHGNAIMTISTTIV	
Db	402 RMVQLEIIT - -DQVMSYGLG - RGAVAYALV - - -VLLDEKRVKEKNLFVSTTIV	
Qy	430 TMVFGMMTKPLIR - LILLPASGHPVTEPSSPKSLH 463	
Db	454 VIFQGLTIRPLVQWLKVKSEH - - -REPKLNEKLH 485	

DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/hydrogen exchanger 1 (Na(+)/H⁺ exchanger 1) (NHE-1).
DE SLC9A1 OR NHE1.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurograthi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
STRAIN=BALB/c;
Dewey M.J., Bowman L.H.;
Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: INVOLVED IN pH REGULATION TO ELIMINATE ACIDS GENERATED
BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
TRANSDUCTION.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- PTM: PHOSPHORYLATED (POSSIBLE).
-!- SIMILARITY: BELONGS TO THE NA(+) / H⁺ EXCHANGER FAMILY.
-!- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
DOMAINS IN THE NA(+) / H⁺ EXCHANGERS VARY AMONG AUTHORS.
-!- CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT BELIEVED TO BE
TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.

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CC mercial entities requires a license agreement. (See <http://www.isb-sib.ch/>)
CC or send an email to license@isb-sib.ch
CC or send an email to license@isb-sib.ch

Best Local Similarity	29.1%	Pred.	No. 4.7e-24;
Matches	147; Conservative	Mismatches	202;
Indels	58;	Gaps	19;
y	18 DYASV--VSINLEVALACTIVLGHLEE-NRWNESTITALIIGLCTGVILLMTKGKS	73	
b	1 : : : : : :		
b	99 DYPHRVTPEISWLLAQLMKPHEVPTTISVYVGLGGLI--FKGV 154		
y	74 SHLFVESEDFFYLPLPIFNAQVKKOPFRNEMTTLFGAVGMISFTPS--IAA 131		
b	1 : : : : : :		
b	155 ETPFLQSDIVFFLPLPPIIDLGYFLPLQFTENLGTILIFAVGTLWNAFLGGLY 214		
y	132 IAFESRMNLTGLDVGDELIGATEFSATDSVCTQLOVLADE-TPFLYSLVFGESVNDATS 190		
b	215 VCLVGGEQINNIGLDTLFGSLSAVDFAVAVFEEHINELHLHVFGESLNLDAVT 274		
y	191 IVLENALQNF--DLVHTDAAVLKVFLGNMFYFLFSLSTPLFGVPGFLSSAYIKKLYIGR 247		
b	275 VVLTHLPIEFASTPSVGI SDTFIPLGFLSEPVYALGVGFVVYGVLAFTSR--FTSH 329		
y	248 STDREVALMMLMAYLTSYMLAFLDLSGLITVFGVMSHTYHNVTESRVYKHFAT 307		
b	330 IRVIEPLFLFELYSTMAYLISAEFLHSIGMALIASGVMPYVEANISHKSHTTIKFIM 389		
y	308 LSFIAETFLFLYLVGMDAL DICKMEFAASDRPKGSIGISSLIGLVLIGRAAFYEPPLSLS 366		
b	390 WSSVSETLIFLFLGVSTVAGSHONWW-----TFVISTL--FCLTIAVLGYLVLTWFI 440		
y	367 NLTKRAPNERKITYWRQCVVTTWAGLMLGRGAVSYIALAYNKFTPSRGHTQLHGNAIMTSTIV 426		
b	441 N--KFKRIVLTPDQFIIAYGGL-RGAFLSGLY-LIDKKKHPMC--LEFTAITTYI 492		
y	427 LFSTMVFGMMTKPLTRLPLASPHPTSEPPSPSKLHSPLLTSMOGSDIESTTNIVRPS 486		
b	493 FFTVYVQGMYLRLPYLDL---AVKKKOETKRSINEEHTQFLDHLTGIEDIC--- 542		
y	487 LRMLLTKPHTVHYYWRKEDDALMR 511		
b	543 -----GHYGHHWK---DKLNR 556		
RESULT 13			
RAH5_RAT			
ID	NAH5_RAT	STANDARD;	PRT;
AC	Q920XZ;		898 AA.
DT	30-MAY-2000 (Rel. 39, Created)		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Sodium/hydrogen exchanger 5 (Na(+)/H(+) exchanger 5) (NHE-5).		
GN	SLC9A5 or NHE5.		
GN	Ratetus norvegicus (Rat).		
DS	Ratetaurao; Chordata; Craniata; Vertebrata; Euteleostomi;		
DC	Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Rattus.		
NCBI_TaxID	10116;		
RN	SEQUENCE FROM N_A.		
STRAIN	Wistar;		
RC	STRAINA_Wistar;		
RR	MEDLINE=991341373; PubMed=9933642;		
RX	Attaphitaya S., Park K., Melvin J.E.;		
CC	"Molecular cloning and functional expression of a rat Na+/H+ exchanger (NHE5) highly expressed in brain."		
CC	J. Biol. Chem. 274:4383-4388 (1999).		
-	FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL TRANSDUCTION (BY SIMILARITY).		
CC	SUBCELLULAR LOCATION: Interastral membrane protein.		
CC	- PTM: PHOSPHORYLATED (POSSIBLE).		
CC	- PTM: HIGHLY EXPRESSED IN BRAIN.		
CC	- SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.		
CC	- CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.		

112

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FT DOMAIN	474	482	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	483	503	M (M10) (POTENTIAL).
FT DOMAIN	504	822	CYTOSPLASMIC (POTENTIAL).
FT CARBOHYD	374	374	N LINKED (GLCNAC, . . .) (POTENTIAL).
FT SEQUENCE	822 AA;	92003 MW;	E97C1ACD4BB8DAA CRC64;
Query Match	17.68;	Score 478;	DB 1; Length 822;
Best Local Similarity	28.78;	Pred. No. 5.5e-201;	Matches 145; Conservative 101; Mismatches 201; Gaps 19;
Qy	18	DYASV---VSINLEVALCIVLGHLEE-NRWNESITALLIGLCTGVILLMTKGKS	73
Db	99	DYLHVRTPPEEISWILACLMKIGFHVPTTSSIVESPCLLIVVGLVGGGLI---KGVG	154
Qy	74	SHLFVFSSEDLFFFLYLPPIIFNAGFOVKKKOFFRFNMITLFGAVTMISFTIS--IAA	131
Db	155	ETPPFLQSDVDFEFLPLTFDAGYFLPRTENLGTILIAVGTGLWNAFFLGLLYA	214
Qy	132	IATFSRMNIGTLDVGDELAIGAIFSASTD SVCTQLVNLNODE-TPELYSLVFEGVVNDATS	190
Db	215	VCLVGGEOINNNGLLDTLGFSTISADPVAVVAFEEIHINELLTVRESLINDAVT	274
Qy	191	IVLENALQ---NFDLVHTDAAVVLKFLGNNFFYLFLSSTFLGYFAGELLSAYIKKLYIGRH	247
Db	275	VVLYHLPEEFANYSDTIGI-SDFLFLGFL-SFFVVAFLGVFVGVYGAFTSR---FTSH	329
Qy	248	STDREVALMLMLAYLSYMLAEELDLDSLTLTYFFCGIVMSHYTWHNNTESRVTKHAFAT	307
Db	330	IRVTEPLFLVFLSYMATLSAELPHLSGTMALIASGVMPVEANISHKSHTTIKYFLKM	389
Qy	308	LSFAETFLFLVYGMDAL-DIEKWEEFASDRPGKSIGISISSLGLVJGRAFYFPLSFLS	366
Db	390	WSSVSETUFLIFLGFVSTVAGSHQWWN-----TFVSTLL--FCLLARVLGVLVLTWFI	440
Qy	367	NLTKKAPNEKITWQVVVWAGLMLGCAVSIALAYNKFTRSCHTQLHGNAMITMITSITVV	426
Db	441	N---KFIVKLTKPKDOFTIAYGGL-RGIAFASGY--LMDKKHFPICD--LFLTLTTVI	492
Qy	427	LFSTMVFRGMMTKPFLRLLPASGHPTSEPSSPKSLSHSPLITSMQGSDLESTTNVTPSS	486
Db	493	FFTVVFVQGMTIRPLVLL-----AVKKQKEFKRSINEEINTQFLDHLTGIEDIC---	542
Qy	487	LRLMLTKPTHTVHYWRFKDDALMR 511	
Db	543	-----GHHGHHWK--DKLNK 556	
RESULT 15			
NAH1_BOVIN	STANDARD;	PRP;	817 AA.
ID NAH1_BOVIN			
QB0306;			
AC			
DT 01-NOV-1997 (Rel. 35, Created)			
DT 01-NOV-1997 (Rel. 35, Last sequence update)			
DT 15-JUN-2002 (Rel. 41, Last annotation update)			
DE Sodium/hydrogen exchanger 1 (Na(+)/H(+)) exchanger 1) (NHE-1).			
DN SLC9a1 OR NHE1.			
OS Bos taurus (Bovine).			
RC TISSUE=Heart;			
RA Zhu H., Zhang Q., Liu W., Trumbly R.J., Garlid K.D.,			
RA Sun X.;			
RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.			
CC -!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL TRANSDUCTION.			
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.			

PTM: PHOSPHORYLATED (POSSIBLE).
SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
NUMBER: LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS, A, B AND L ARE NOT BELIEVED TO BE TRANSMEMBRANAL, BUT ONLY MEMBRANE ASSOCIATED.
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EMBL: U49432; AAA91483-1;
InterPro: IPR00676; Nah_Exchngr.
InterPro: IPR004709; Nah_Exchanger_1.
PFam: PF00999; Na_H_Exchanger_1.
PRINTS: PRO1084; NAEXCHNGR.
TIGRFAMS: TIGR00840_bcpal; 1.
DR Transmembrane; Glycoprotein; Transport; Antiport; Sodium transport; Multigene family; Phosphorylation.
KW KW
DOMAIN 1 15
FT TRANSMEM 16 35
FT DOMAIN 36 107
FT TRANSMEM 108 127
FT DOMAIN 128 129
FT TRANSMEM 130 149
FT DOMAIN 150 154
FT TRANSMEM 155 174
FT DOMAIN 175 191
FT TRANSMEM 192 211
FT DOMAIN 212 227
FT TRANSMEM 228 247
FT DOMAIN 248 256
FT TRANSMEM 257 276
FT DOMAIN 277 294
FT TRANSMEM 295 315
FT DOMAIN 316 338
FT TRANSMEM 339 358
FT DOMAIN 359 386
FT TRANSMEM 387 406
FT DOMAIN 407 410
FT TRANSMEM 411 430
FT DOMAIN 431 480
FT TRANSMEM 481 500
FT DOMAIN 501 817
CARBOHYD 75 75
CARBOHYD 370 370
SEQUENCE 817 AA; 91017 MW; 6617893B012920 CRC64;
Query Match Score 476; DB 1; Length 817;
Best Local Similarity 28.8%; Pred. No. 7.4e-24;
Matches 146; Conservative 98; Mismatches 201; Indels 62; Gaps 19;

Qy 18 DYASV--VSTNLFLVALLCACLVLGHLEE NRWNNESTPALIIGLCTGVVLLMTKGKS 73
Db 95 DYQHVRIPPEEALWLLIACLMKIGFHVPTLSSIVESPCLLIVVGLVGGGLI---KGVG 150
Qy 74 SHLFVFSEDLFIFTLLPPTIFNAGFOVKKKOFFRFNMITLFGAVTMISFTIS--IAA 131
Db 151 ETPPILLOSEVFLPLPPIILDAGFLPLQFTENLGTILFAVVGTLWNAFFGLGLMYA 210
Qy 132 IAIFSRMNIGTLDVGDFLAIGAIFSATDSVCTQLVNLQDE-TPELYSLVFGVYNDATS 190
Db 211 VCLVGGEOINNNGLLENLFLFGTSISAVDPVAVLVEEIHINELLVPGESLNDAVT 270
Qy 191 IVLFINALQ--NFDLVHIDAIVLKKFLGNNFFYLFLSSTFLGYFAGLSSAYIKKLYIGRH 247
Db 271 VVLYH1FEFANYDRVGI-VDLIGFL-SFFVVSLLGVEFVGVYTAFTSR--FTSH 325
Qy 248 STDREVALMLMLMAYLSYMLAEELDLDSLTLTYFFCGIVMSHYTWHNNTESRVTKHAFAT 307

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Db 326 TRVIEPLFLVFLYSYMAYLSAELFHSGIMALIASGVYMRPVEANISHKSHTTIKYFLKM 385
Qy 308 LSFIAETFLFYVGMDALDIE--KWEFASDRPGKSGISSLGLVLIGRAAFVPLSF 364
Db 386 WSSVSETLIFLGVSTVAGSHWNNTFV-----ISTPL--FCLIAVVLGVGLTW 434
Qy 365 LSNLTKKAPNEKITWROQQVVIWAGLMRGAVIALAYNKFRSGHTQLHGNAIMTSTIT 424
Db 435 FTN---KFRIKLTPKDQFIAYGGL-RGAIAFSLGY-LIDKKHPPMCD-LFLTAIT 486
Qy 425 VVLFSTMVFGMTKPLTRLLIPASGHPTSSPSSPKSLHSPLLTSMQGSDLESTTNIVRP 484
Db 487 VIFFTYFVOGHTIRPLYDLL----AVKKQETKRSINEEHTQFLDHLLTGIEDIC-- 538
Qy 485 SSLRMLLTkpHTVARYWRKDDALMR 511
Db 539 -----GHYGHHHWK--DKLNR 552

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search completed: March 26, 2003, 18:53:06
job time : 34 secs

Db	61	TGVVILIMTKSSHLFVSSDLFFYLPPIIFNAGFOVKKQFRNFMTITLFGAVGT	120		Qy	127	ISIAIAIAIFSRMNIGTIDVGDFLAIQAIIFSAIDSVCILQLQVLNQDETFPLYSLVFGGVVN	186
Oy	121	MISFFTISIAIAIFSRMNIGTIDYGFDFLAIQATISATSDCTVCLQVLNQDETFPLYSLVF	180		Db	129	ISLGALSIFFKLIDIGLIELADYLAQAIIFAAIDSVCILQLQVNQDETFPLYSLVFGGVVN	188
Db	121	MISFFTISIAIAIFSRMNIGTIDYGFDFLAIQATISATSDCTVCLQVLNQDETFPLYSLVF	180		Qy	187	DATSTVLFNALQNFDLVHDAAVVLFGLVFAEGLSAYIKKLYIGR	246
Oy	181	GEGVNDATSVLFLNALQNFDLVHDAAVVLFGLVFAEGLSAYIK	240		Db	189	DATSVLFNALQSFDFLRIDHRIALQMGNFNLFTASLILGAFTGILSAYIKKLYIGR	248
Db	181	GEGVNDATSVLFLNALQNFDLVHDAAVVLFGLVFAEGLSAYIK	240		Qy	247	HSTDREVALMMLMAYLSYMLAELLDLSGLTIVFCGIVMSHYTWHNTESSRVTKHAF	306
Oy	241	KLYIGRHSTREVALMMLMAYLSYMLAELLDLSGLTIVFCGIVMSHYTWHNTESSRV	300		Db	249	HSTDREVALMMLMAYLSYMLAELDFLYLSGLTIVFCGIVMSHYTWHNTESSRVTKHAF	308
Db	241	KLYIGRHSTREVALMMLMAYLSYMLAELLDLSGLTIVFCGIVMSHYTWHNTESSRV	300		Qy	307	TLSFIATFLFLYLVGMDALDIEKEWPAEDRGPKSIGISSLLGLYLGRAFVPLSFLS	366
Oy	301	TKHAPATLSFAETFLFLYGMDALDIEKEWPAEDRGPKSIGISSLLGLYLGRAAFV	360		Db	309	TLSFIATFLFLYLVGMDALDIEKEWPAEDRGPKSIGISSLLGLYLGRAFVPLSFLM	368
Db	301	TKHAPATLSFAETFLFLYGMDALDIEKEWPAEDRGPKSIGISSLLGLYLGRAAFV	360		Qy	367	NLTKIKAPNEKITWROQVTVWAGLMRGAVALTAYNKFTRSQHTOLHGNAIMIT	426
Oy	361	PLSFLSNLTKAPNEKITWROQVTVWAGLMRGAVALTAYNKFTRSQHTOLHGNAIMIT	420		Db	369	NFAKSQSSEKVTENQOVIWVAGLMRGAVALNQFTRSQHTOLHGNAIMITSISVV	428
Db	361	PLSFLSNLTKAPNEKITWROQVTVWAGLMRGAVALTAYNKFTRSQHTOLHGNAIMIT	420		Qy	427	LFSIATVFGMMTKPLTRLIPASGH-- -PVTSSEPSPKSLHSPLITSQGSDL	475
Oy	421	STIVVLFSTMVFGMMTKPLTRLIPASHPVTSFSPSSPKSLHSPLITSQGDSLESTN	480		Db	429	LFSIATVFGJLTKPLTRLIPASHPVTSFSPSKYSLPREGNDQEYDVGNGNH	488
Db	421	STIVVLFSTMVFGMMTKPLTRLIPASHPVTSFSPSSPKSLHSPLITSQGDSLESTN	480		Qy	476	ESTT-- -NIVRPSSRLMLLTKPHTHVYWKFDALMRPMFGGFVPFSPGSPTEQS	531
Oy	481	IVRPSSLRMILLTKPTHTHVYWKFDALMRPMFGRGEVPFSPGSPTEQS	535		Db	489	EDTTPRTIVRPSLRLMLLNAPHTVHYWKFDALMRPMFGRGEVPFSPGSPTEQS	547
Db	481	IVRPSSLRMILLTKPTHTHVYWKFDALMRPMFGRGEVPFSPGSPTEOSSHGR	535					
				RESULT 3				
				Q94LY5				
				ID	Q94LY5			
				PRT:	PRELIMINARY;			
					PRT:	540 AA.		
				AC	Q94LY5;			
				DT	01-DEC-2001	(TREMBLrel. 19, Created)		
				DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)		
				DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)		
				DE	Na-H_antIportor	.		
				DE	Na/H_antIportor	Nhx1.		
				GN	AGNIXII.			
				OS	Atriplex_gmelini.			
				OC	Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
				OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
				OC	Asteridae; easterids I; Solanales; Solanaceae; Petunia.			
				OX	NCBI_TaxID=4102;			
				RN	[1]			
				RP	SEQUENCE FROM N.A.			
				RA	Iida S., Kusumi T., Yonekura-Sakakibara K., Tanaka Y.;			
				RT	"Plant Na-H antipor,"			
				RL	Submitted (Nov-2000) to the EMBL/GenBank/DBJ databases.			
				DR	EMBL: AB051817; BA56105.1; -.			
				DR	InterPro: IPR000676; FKB_PPIase.			
				DR	InterPro: IPR000676; Nah_Exchanger.			
				DR	Pfam: PF00999; Na_H_Exchanger.			
				DR	PROSITE: PS00453; FKB_PPIASE_1; UNKNOWN_1.			
				DR	SEQUENCE: 540 AA; 59510 MW; BCE2740F275E806A CRC64;			
				DR	Query Match Score 77.3%; Score 2103.5%; DB 10; Length 540;			
				DR	Best Local Similarity 77.4%; Pred. No. 3.2e-147;			
				DR	Matches 40; Conservative 53; Mismatches 62; Indels 3; Gaps 1;			
				DR	16 STSDHQSVVNSINLVALFQVNLVALCIVLGHLEENRMNESITALVSGCTGVILLISGGNS 75			
				DR	75 HLFVSEDFLFFYLPPILFNAQFQVKKKOFFRFNTITLFGAVGMISFTISIAIAI 134			
				DR	16 HLFVSEDFLFFYLPPILFNAQFQVKKKOFFRFNTITLFGAVGMISFTISLGAIGI 135			
				DR	135 FSRMNIGTIDVGDFLAIQAIIFSAIDSVCILQLQVNQDETFPLYSLVFGGVVN DATSYLF 194			
				DR	67 LMTKGKSHLFFSEDFLFFYLPPILFNAQFQVKKKOFFRFNTITLFGAVGMISFT 126			
				DR	69 LITGGKSHLFFSEDFLFFYLPPILFNAQFQVKKKOFFRFNTITLFGAVTLVSYFTI 128			
				DR	195 NALQNFDFLVDLVAFLVHDAAVVLFGLGNFNFYLFLSSTSFLGVAGLLSAYIKKLYIGRHSTDREVA 254			

RP	SEQUENCE FROM N.A.	RN	[1]	SEQUENCE FROM N.A.
RC	STRAIN=PR-R; TISSUE=LEAF;	RP		
RX	MEDLINE=212/666; PubMed=11382810;	RA	Zhang H., Zhang Q., Ma X.;	
RA	"Na ⁺ /H ⁺ antipporter in Suaeda salsa.";	RT	"Na ⁺ /H ⁺ antipporter in Suaeda salsa.";	
RA	Yamaguchi T., Fukada-Tanaka S., Inagaki Y., Saito N.,	RL	Submitted (APR 2001) to the EMBL/GenBank/DBJ databases.	
RA	Yonekura-Sakakibara K., Tanaka Y., Kusumi T., Iida S.;	DR	EMBL; AF370358; AAC53412.1;	
RT	"Genes Encoding the vacuolar Na ⁺ /H ⁺ Exchanger and Flower Coloration."	DR	InterPro; IPR001179; FKBPP_Ptase.	
RL	Plant Cell Physiol. 42:451-461 (2001).	DR	InterPro; IPR004709; Nah_Exchanger_3.	
DR	EMBL; AB031990; BAB16381.1;	DR	InterPro; IPR006167; Nah_Exchanger_1.	
DR	EMBL; AB03399; BAB16380.1;	DR	IPR006167; Nah_Exchanger_1.	
DR	EMBL; AB055062; BAB0899.1;	DR	Pfam; PF00999; Na_H_Exchanger_1.	
DR	InterPro; IPR001179; FKBPP_Ptase.	DR	TIGRFAMS; TIGR00810; b_cpf1; 1.	
DR	InterPro; IPR004709;	DR	PROSITE; PS00453; FKBPP_Ptase_1; UNKNOWN_1.	
DR	InterPro; IPR006167; Nah_Exchanger_3.	DR	SEQUENCE; 556 AA; 61672 MW; DDF6AB967647D48E CRC64;	
DR	PRINTS; PRO1084; NAHEXCHNGP.	Query Match	75. 5%	Score 2054. 5; DB 10; Length 556;
DR	TIGRFAMS; TIGR00840; b_cpf1; 1.	Best Local Similarity	74.28;	Pred. No. 1.4e-143;
DR	PROSITE; PS00453; FKBPP_Ptase_1; UNKNOWN_1.	Matches	395;	Mismatches 56; Indels 13; Gaps 2;
SQ	SEQUENCE 54.2 AA; 59973 MW;	Query	13 LYPTSDYASVYSTNLFEVALLCACIVLGHILEENRWVNESITALLIGLCTGVVLLMTKGK 72	
Query	16 TSDYASVVSINLFVALAACIVLGHILEENRWVNESITALLIGLCTGVVLLMTKGSSH 75	Db	MVSPSDHASVVSMLFVALLRGCVTIGHILEENRWVNESITALLIGLCTGVVLLMTSGK 74	
Matches 401; Conservative 49; Mismatches 66; Indels 9; Gaps 3;	Db	SSHLFVFESDLFFYLPLPPIFNFGQYKKQFFERNPNTILFGAVGMISFTSIAAI 132		
Db	16 TSDHASVVSINLFVALAACIVLGHILEENRWVNESITALLIGLCTGVVLLMTSGKSH 75	Db	SSHLFVFESDLFFYLPLPPIFNFGQYKKQFFERNPNTILFGAVGMISFTSIAAI 132	
Query	76 LFFVFSDEDLFFYLPLPPIFNFGQYKKQFFERNPNTILFGAVGMISFTSIAAI 135	Db	AIFSMNIGLTGDLAFLGAIAFISATDSVCTLQVLYNQDETFLYSLVGEVYNDATSV 192	
Db	76 LLYFSESDLFFYLPLPPIFNFGQYKKQFFERNPNTILFGAVGMISFTSIAAI 135	Db	135 AIFMDIGLSLELDLLAIGAIFATDSVCTLQVLYNQDETFLYSLVGEVYNDATSV 192	
Query	136 SRMNIGLTGDLAFLGAIAFISATDSVCTLQVLYNQDETFLYSLVGEVYNDATSVLFN 195	Db	135 LFNALQNFOLVHIDAVYLKFLGNFPEYLFLSSTFLGVFAGLSSAYIKKLYIGRHSTDRE 252	
Db	136 KHDIDPDLFGYLAIGAIAFATDSVCTLQVLYNQDETFLYSLVGEVYNDATSVLFN 195	Db	135 LFNALQNFOLVHIDRAIAFGGGNLYLFFASTFLGVFAGLSSAYIKKLYIGRHSTDRE 252	
Query	196 ALQNFDLVHIDAAVVLKFGLNNFFYLFLSSTFLGVFAGLSSAYIKKLYIGRHSTDREVAL 255	Db	136 LFNALQNFOLVHIDRAIAFGGGNLYLFFASTFLGVFAGLSSAYIKKLYIGRHSTDRE 252	
Db	196 AIQSFDMTSDFPKIGLHFIGNFLYLFLSSTFLGVFAGLSSAYIKKLYIGRHSTDREVAL 255	Db	136 LFNALQNFOLVHIDRAIAFGGGNLYLFFASTFLGVFAGLSSAYIKKLYIGRHSTDRE 252	
Query	256 NMMLMAYSYMIAELLDISGLTIVFEGVIMSHYTHWNTESSRVTTKHAFTLSPJA 315	Db	136 LFNALQNFOLVHIDRAIAFGGGNLYLFFASTFLGVFAGLSSAYIKKLYIGRHSTDRE 252	
Db	256 NMMLMAYSYMIAELLDISGLTIVFEGVIMSHYTHWNTESSRVTTKHAFTLSPJA 315	Db	136 LFNALQNFOLVHIDRAIAFGGGNLYLFFASTFLGVFAGLSSAYIKKLYIGRHSTDRE 252	
Query	316 LFIVGMDALDIEKWEPAFDREGPSKGSLGIGSIIISLGLVLIBGRAFVEPLSLSNLNTKAPNE 375	Db	136 LFNALQNFOLVHIDRAIAFGGGNLYLFFASTFLGVFAGLSSAYIKKLYIGRHSTDRE 252	
Db	316 LFIVGMDALDIEKWEPAFDREGPSKGSLGIGSIIISLGLVLIBGRAFVEPLSLSNLNTKAPNE 375	Db	136 LFNALQNFOLVHIDRAIAFGGGNLYLFFASTFLGVFAGLSSAYIKKLYIGRHSTDRE 252	
Query	376 KITWRRQQVVIWAGLMRGAVALAYNKTFRTSGHTOLQHGNAIMITSTTVVLFSTMVFGM 435	Db	136 LFNALQNFOLVHIDRAIAFGGGNLYLFFASTFLGVFAGLSSAYIKKLYIGRHSTDRE 252	
Db	376 KITSRQQTIIWAGLMRGAVALAYNKTFRTSGHTOLQHGNAIMITSTTVVLFSTMVFGM 435	Db	136 LFNALQNFOLVHIDRAIAFGGGNLYLFFASTFLGVFAGLSSAYIKKLYIGRHSTDRE 252	
Query	436 MTKPLIRLLP----ASGH----VTESEPPSSPKSLHSPPLTSMSQDPLEST--NIVRPPSS 486	Db	136 LFNALQNFOLVHIDRAIAFGGGNLYLFFASTFLGVFAGLSSAYIKKLYIGRHSTDRE 252	
Db	436 MTKPLINLLPQPHQKOMESGHSSMMTSSPSSPHFTPLQDQPSMDSMITIGPEVARTA 495	Db	136 LFNALQNFOLVHIDRAIAFGGGNLYLFFASTFLGVFAGLSSAYIKKLYIGRHSTDRE 252	
Query	487 LRMLLTKTHVHYWKFDALMRPMGGFGRFVPPSPGSPEQS 531	RESULT 9		
Db	496 LRMLLRTPTHTVHYWKFDALMRPMGGFGRFVPPSPGSPEQS 540	Q9ARH6		
Q9*K25	PRELIMINARY;	AC	Q9ARH6; PRELIMINARY;	
ID Q94K25		DT	01-JUN-2001 (TREMBLrel. 17, Created)	
AC Q94K25;		DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT 01-DEC-2001 (TREMBLrel. 19, Created)		DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)	
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)		DE	Sodium/proton exchanger.	
DE Na ⁺ /H ⁺ antipporter.		OS	Citrus paradisi (Grapefruit).	
OS Suaeda maritima subsp. salsa.		OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC Eukaryota; Magnoliophyta; eu dicotyledons; core eudicots;		OC	Spermatophyta; Magnoliophyta; eu dicotyledons; core eudicots; Rosidae;	
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Suaeda.		OC	eurosid s II; Sapindales; Rutaceae; Citrus.	
NCBI_TaxID=126914;		OX	NCBI_TaxID=37656;	
RN SEQUENCE FROM N.A.		RN	SEQUENCE FROM N.A.	
RP		RP		
RC		RC		
TISSU=PEEL.		TISSU=PEEL.		
RA Porat R., Lurie S., Povancello D.;		RA		
RT "A heat treatment induced the transcription of a sodium proton		RT		

RT	function in cation detoxification in yeast.";
RL	Submitted (OCT-2001) to the EMBL/GenBank/DDJB databases
DR	EMBL; AY028116; AAK27314.2; -.
DR	InterPro; IPR001179; FKBP_PPIase.
DR	InterPro; IPR004709; NaH_Exchange3.
DR	InterPro; IPR00676; NaH_Exchanger.
DR	PFam; PF00599; Na_H_Exchanger_1.
DR	PRINTS; PRO1084; NAHXCHNRR.
DR	TIGRFAMS; TIGR00840; b_cpal1; 1.
DR	PROSITE; PS00454; FKBP_PPIASE_1; UNKNOWN_1.
SO	SEQUENCE 542 AA; 59836 MW; 1A8525F2C5FAEEDC CRC64;
Query Match	75.1%; Score 2043; DB 10; Length 542;
Best Local Similarity	74.3%; Pred. No. 9.3e-143;
Matches	394; Conservative 57; Mismatches 71; Indels 8; Gaps 4;
Db	13 SHLEPVFSEDLFFIYLPPFLNAGFQVKKQFFRNEMTILFGAVGTMISSFTLISIAAI 132
Db	74 SHLEPVFSEDLFFIYLPPFLNAGFQVKKQFFRNEMTILFGAVGTMISSFTLISLGVI 133
Qy	133 AIFSRMNIGLTDVGDELAIALFATSDVCTQLQVINQDETFPLFLSVLFGGVNDATSI 192
Db	134 QFFKLDIGLTDIGDLYLAIGIAFATAATSDVCTQLVNQDDTPFLYSVLFEGGVNDATSWV 193
Qy	193 LFNALQNFELVHIDAAVVLFLGNNFLFLLSTFLGVFAGLSAYIKKLYIGRHSTDRE 252
Db	194 LEFNAQSFDLTHINTRSAFOLGFLNQFLGFLPFLTGIVGLSAYIKKLYIGRHSTDRE 253
Qy	253 VALMMLMAYLSYMELDLDSLGIITVFCCGIVMSHYTWNVTESSRVTTKHAFTLSETA 312
Db	254 VAIMVLMAYLSYMELFLYLSGILITVFCCIVMSHYTWNVTESSRVTTKHAFTLSETFA 313
Qy	313 ETFLFLYVGMDALDIKEWFAASDRPGKSIGISSLILGVLYLGRAFAFPFLSFLSNTTKA 372
Db	314 EIFTFLYVGMDALDIKEWRAVKKGSPGTSYAASAMLMGLIMAGRAFAFPFLSFLNLAKKS 373
Qy	373 PNEKLTWRQOVVWAGLARGAVSTALANKFTTSQHTQLHGNALIMITSTTVLFSIMV 432
Db	374 PTEKISIKQOQVTVWAGLNRGAWSMALYNOTFSGHTQLRENAMEITSTTVLFSIVV 433
Qy	433 FGMMTKPLTRLLPASGHP --VTPSPSKPLHSPLTSMOG --SDLESITNIVRPS 486
Db	434 FGLMTEPLRLLHPKPKHTNHLISDPSTPKSLSQLLEGGQDQDSYADLVGPT -VPRPGS 492
Qy	487 LRMLLTKPTHTVHYWKRKFDDALMRPMFGRGYFPEPSGPSPTEQS -HGGR 535
Db	493 LRALLTPPTHTVHYWKRKFDDAFMRPVFGRRGFAFVPGSPTERSVRGGQ 542
RESULT 10	SEQUENCE FROM N_A.
O9ZPK3	PRELIMINARY; PRT; 538 AA.
ID	Q94LX3
AC	Q94LX3; PRELIMINARY; PRT; 555 AA.
DT	01-MAY-1999 (TREMBrel. 10, Created)
DT	01-JUN-2000 (TREMBrel. 21, Last sequence update)
DE	Sodium proton exchanger NHX1 (Fragment).
GN	NHE1.
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicots; Rosidae;
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID	3702;
RN	[1]
RP	SEQUENCE FROM N_A.
RC	STRAIN=CV_COLUMBIA;
RX	MEDLINE=9145575; Pubmed=9996049;
RA	Gaxiola R.A., Rao R., Sherman A., Grisafi P., Alper S.L., Fink G.R.;
RT	"The Arabidopsis thaliana proton transporters, AtNHx1 and Avp1, can
RT	function in cation detoxification in yeast.";
RL	Proc. Natl. Acad. Sci. U.S.A. 96:1480-1485(1999).
RN	[2]
RP	SEQUENCE FROM N_A.
RA	Quintero F.J., Blatt M.R., Pardo J.M.;
RT	"The AtNHE1 gene encodes a putative Na+/H+ antiporter."
RL	Submitted (MAR-1998) to the EMBL/GenBank/DDJB databases.
DR	EMBL; AF106224; AAD16046.1; -.
DR	EMBL; AF056190; AAF217155.1; -.
DR	InterPro; IPR001179; FKBP_PPIase.
DR	InterPro; IPR004709; NaH_Exchange3.
DR	InterPro; IPR00676; NaH_Exchanger.
DR	Pfam; PF00599; Na_H_Exchanger_1.
DR	PRINTS; PRO1084; NAHXCHNRR.
DR	TIGRFAMS; TIGR00840; b_cpal1; 1.
DR	PROSITE; PS00454; FKBP_PPIASE_1; UNKNOWN_1.
FT	PROSITE; PS00453; FKBP_PPIASE_1; UNKNOWN_1.
SQ	538 AA; 59513 MW; 1A89AD6C5C726996 CRC64;
Query Match	74.3%; Score 2023.5; DB 10; Length 538;
Best Local Similarity	73.3%; Pred. No. 2.5e-141;
Matches	389; Conservative 60; Mismatches 79; Indels 3; Gaps 2;
Db	2 LDLSYKLPSL-STSDHASVANLFLVALCACIVLGHLEENRNNESTITALIGLCTG 62
Qy	3 MEVAARGLALYTTSDASYVSINLFLVALCACIVLGHLEENRNNESTITALIGLCTG 62
Db	61 VTILLISKGSLLIVSEDIFTYLPPFLIFNAGQVKKQFFRNEMTITLFGAVGTMI 122
Qy	63 VVILIMTKGKSSHLFVESEDIFFYLPPFLIFNAGQVKKQFFRNEMTITLFGAVGTMI 122
Db	61 VTILLISKGSLLIVSEDIFTYLPPFLIFNAGQVKKQFFRNEMTITLFGAVGTII 120
Qy	123 SFETISIAATAIFSRMNIGLTDVGDFPLAIGAFISATDSVCTQLVNQDETFLFLYSLVGE 182
Db	121 SCTIISLGVTFQFKLIDGFLGDLYLAIGAFIAATDSVCTQLVNQDETFLFLYSLVGE 180
Qy	183 GVVDATSTVFLNALQNFDLVHIDAVVLFLGNNFLYFLSFLSTFLGFLAGILSAYIKKL 242
Db	181 GVVDATSTVFLNALQSFDLTHLNHEAFHULGFLYFLSFLSTLGAATGLISAVIKKL 240
Qy	243 YIGRSIDREVAMLMAYLSYMELDSLISGILITVFCGIVMSHYTWNVTESSRVTTK 302
Db	241 YFGRSIDREVAMLMAYLSYMELDSLISGILITVFCGIVMSHYTWNVTESSRVTTK 300
Qy	303 HAFATLFLTAETFLFLYVGMDALDIKEWFAASDRPGKSIGISSLILGVLYGRAFVFPL 362
Db	301 HTFATLFLAETFLFLYVGMDALDIKEWFAASDRPGKSIGISSLILGVLYGRAFVFPL 360
Qy	363 SFLSNLTKAPNEKLTWQRQVIVWAGLARGAVSTALAKFTTSQHTQLHGNALIMITST 422
Db	361 SFLSNLAKNOSEKINFNMQCVIVWMSGLVRGAWSMALAKFTTRAGHTDVRGNALIMITST 420
Qy	423 ITVWLFLSTWFGMATTKPLRLLPASGHVIT - SEPSPSKSLHSPLTSQGSDEESTITN 480
Db	421 ITVCFLSTVVGMLTKPLISYLPHONATSMISDDNTPKSITHIPLQDQSFTEPSGNHN 480
Qy	481 VPRFDSTRGFLTRTWHYVWRFDAFLMRPMFGGRGYFVPSGPSPTEQS 531
Db	481 VPRFDSTRGFLTRTWHYVWRFDAFLMRPMFGGRGYFVPSGPSPTEQS 531
RESULT 11	SEQUENCE FROM N_A.
Q94LX3	Torenia hybrida.
ID	Q94LX3
AC	Q94LX3; PRELIMINARY; PRT; 555 AA.
DT	01-DEC-2001 (TREMBrel. 19, Created)
DT	01-DEC-2001 (TREMBrel. 19, Last sequence update)
DT	01-JUN-2002 (TREMBrel. 21, Last annotation update)
DE	Na_H_Antiporter.
GN	THIPURPLE.
OS	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicots; Rosidae;
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID	3702;
RN	[1]
RP	SEQUENCE FROM N_A.
RC	TheArabidopsis thaliana proton transporters, AtNHx1 and Avp1, can
RX	"TheArabidopsis thaliana proton transporters, AtNHx1 and Avp1, can
RA	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
RT	Asteridae; euasterids I; Lamiales; incertae sedis; Toreniae;

RN [2] SEQUENCE FROM N.A.
 RP SPAIN=CV. COLUMBIA;
 RC Wash-U;
 RA "The A. thaliana Genome Sequencing Project."
 RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RL [3] SEQUENCE FROM N.A.
 RN SEQUENCE FROM N.A.
 RP SPAIN=CV. COLUMBIA;
 RA Waterston R.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF007271; AAB61069_1;
 DR InterPro; IPR01179; FBPP_DPIase.
 DR InterPro; IPR00676; NAH_Exchanger.
 DR Pfam: PF00999; Na_H_Exchanger_1.
 DR PROSITE; PS00453; FBPP_PPIASE_1; UNKNOWN_1.
 SQ SEQUENCE 457 AA: 50611 MW: 0AF2235F1A258EE CRC64:

Query	Match	Length
Qy	62.4% Score 1698.5; DB 10; Length 457;	
Matches 333; Conservate 45; Mismatches 51; Indels 21; Gaps 3;		
Db	2 LDSLVSKPLS_STDSHSSVALNLVALLGACIVLGHLEENRNNNESTALLGLGTG 60	
Qy	63 VVILLMTKGKSSHLYFSEDLFLFYLLPILFNAGFOVKKKOFFRNEMTTLFAGVTMI 122	
Db	61 VTLILISGKSSHLVSEDLFLFYLLPILFNAGQVKKKQFFRNEMTTMLFGAVGTI 120	
Qy	123 SFTTISTATAIALFSRMNIGTDVGDFLIGAIFSATDSVCTLQLVNQDETPFLYSLVGE 182	
Db	121 SCTTISLGYTOFKKLDTGFDGLDYLIGAFAATDSVCTLQLVNQDETPFLYSLVGE 180	
Qy	183 GVNDATSVLNALQNFDLVHDAAVVLFGLGSNFYFLFLSTFLGV-----F 230	
Db	181 GVNDATSVVVNAIQSFDLTHUNHEAAFLLGNFLYFLFLSTLGAASVLFLSSLPFL 240	
Qy	231 AGLLSATIKLYIG-----RHSTDREVALMMLMAYLSYMLAELLDLSGILTTFFCG 282	
Db	241 TGLISAYTIKKLYFGRMFHINCRHSTDREVALMMLMAYLSYMLAELDSGILTTFFCG 300	
Qy	283 IVMSHYWHNVNTESSRVTKHAFATLSFIAETFLFLYGMDALDETEKWEFASDRPGKSIG 342	
Db	301 IVMSHYWHNVNTESSRVTKHAFATLSFIAETFLFLYGMDALDIDKWRVSVDPTPSIA 360	
Qy	343 ISSILGLVLGRAAFYFLSFLSNTLTKAPNEKITWQQVVIWAGLMRCAVSIALYN 402	
Db	361 VSSLTMGLVMGRMVAAYFPEPLSFLSNTLAKKNOSEKINFNMQVVIWWSGLMRGAVSMALAYN 420	
Qy	403 KFRSGHITQLGNAIMITSTTVLFSTMV 432	
Db	421 KFRAGHTPDVRGNAMITSTTVCLFSTMV 450	

Search completed: March 26, 2003, 18:53:48
 Job time : 41 secs

